

CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, e.g. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.

Q Sequence
 Q 9 AA;

31-AUG-1992; US-938334.
26-MAR-1993; US-037230.
07-JUN-1993; US-073103.
(LUDW.-INST CAN)
Boon-failleur, T. De Plan,
van Derbruggen, P.

PR 31-AUG-1992; US-S38334.
 PR 26-MAR-1993; US-07230.
 PR 07-JUN-1993; US-073103.
 PA (LUDW-) LUDWIG, INST CANCER RES.
 PI Boon-falleur T., De Plaen E,
 PI Van Denburghen P.,
 PI Lurquin C, Traversari C;

```

Query Match      100.0% Score 52; DB 1; Length 9;
Best Local Similarity 100.0% Pred. No. 1.5e+05;
Matches         9; Conservative 0; Mismatches 0; Indels 0; Gap 0;

Y   1 EADPTGHSY 9
|   ||||| | |
b   1 EADPTGHSY 9

ESULT      3
D R47330 standard; Protein; 9 AA.

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N-PSDB; Q45/L1.
New nonapeptide derived from tumour rejection antigen precursor - presented by HLA-A1 cancer cells, for use in diagnosis or therapy of esp.: melanoma and breast cancer.

Disclosure: Page 19, 33pp.; English.

An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-Pro-Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen precursor encoded by the MAGE-3 gene and presented by HLA-A1. The nonapeptide can be used in a vaccine to treat a cancerous condition involving HLA-A1 subtype cancerous cells. The nucleic acid encoding the nonapeptide can be used as a probe to identify tumour cells. This sequence is homologous to the peptide described and is encoded by the MAGE-1 gene.

C N 31-AUG-1994 (first entry)
 C HLA-A1 MAGE 1 antigen peptide fragment 161-169
 C Immunogenic; HLA-A1; 2; HLA-A1; HLA-A1; binding motif; MHC molecule
 C immune response; viral infection; cancer; prostate cancer; lymphoma
 C hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
 C Synthetic.
 S W09403205 A.
 D 17-FEB-1994.
 F 06-AUG-1993; U07421.
 R 07-AUG-1992; US-956666.
 R 05-MAR-1993; US-027746.
 R (CYTEK) CYTEL CORP.
 I Cells E, Grey HM,
 R Kubo RT, Sette A;
 R PPI; 94-065405/08.
 T Peptide which specifically binds selected MHC allele - used to
 T induce an immune response for treatment or prevention of viral
 T infection or cancer, or for diagnosis
 S Examp 8; page 52; 150pp; English.
 C The sequences given in R47304-33 and R49201-44 are immunogenic
 C peptides which have a HLA-A3.2, HLA-A1 binding motif.
 C These peptides may be used in the composition of the invention.
 C These peptides are capable of binding selected MHC molecules and
 C inducing an immune response. They can be used to treat and/or
 C prevent viral infection and cancer, e.g. prostate cancer, lymphoma,
 C hepatitis or AIDS. They can also be used to produce antibodies for
 C use as diagnostic or therapeutic agents. The peptides can also be
 C used as diagnostic agents.

Query Match Best Local Similarity 100.0%; Score 52; DB 1; Length 9;

Example 34: Page 336; 10PP; English
 R6375 is a synthetic peptide derived from exon 3.1 of melanoma antigen-1 (MAGE-1), it was used to transfer antigen-E cytolytic T lymphocyte sensitivity to normally non-sensitive cells.

1 EADPTGHSY 9
| | | | | | |
1 EADPTGHSY 9

Query Match	Score 52;	DB 1;	Length 9;
est Local Similarity	100.0%	Pred. No.	1.5e-05;
datches	100.0%	No.	Microphones
o. Conserative	0.	No.	Treadles
		No.	Canister

RESULT 4
50281 D R50281 standard; Protein: 9 AA.
C R50281;
T 26-SEP-1994 (first entry)
W MAGE 1 peptide.
W MAGE: nonapeptide; cancer; melanoma; breast cancer; HLA;
W histocompatibility; human leucocyte antigen; probe; treatment;
W histocompatibility; vaccine.

1 EADPTGHSY 9
 | | | | | | | |
 1 EADPTGHSY 9

 BUILT 6
 5135 R65135 standard; peptide; 9 AA.
 R65135

S
WO9105304-A.
Synthetic A.
WO9105304-A.
D 17-APR-1991.
D 30-APR-1993. NOR157

MAGE 1: immunogenic peptide A01.
 MAGE 1: immunogenic peptide A01; cytotoxic C cells;
 in vitro: immunogenic. A01c: bacterial infections;
 in vitro: immunogenic. A01c: cancer. A01c: bacterial infections;
 malaria.

KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.
 PN WO9504817-A.
 PD 16-FEB-1995.
 PF 01-AUG-1994; U08672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Celis E., Kubo R., Serra H., Tsai V., Wentworth P;
 DR WPI: 95-090895/12.
 PT In vitro activation of cytotoxic T cells for selected killing of
 target cells - for treating e.g. cancer, AIDS, hepatitis etc. by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide
 PS Example 3; Page 38; 53pp; English.
 CC R65109 R65115 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of cytotoxic T cells (CTC).
 CC This is achieved by incubating the CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 Sequence 9 AA;

Query Match Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 7
 R70909 ID R70909; standard; Protein; 309 AA.
 AC R70909.
 DR 09-OCT-1995 (first entry)
 DE Human melanoma antigen MAGE-1.
 KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
 KW HLA-restricted cytotoxic T-lymphocyte activity.
 OS Homo sapiens.
 PN WO9504542-A.
 PD 16-FEB-1995.
 PF 02-AUG-1994; U08721.
 PR 06-AUG-1993; US-103623.
 PA (CYTE-) CYTEL CORP.
 PI Fikes JD, Livingston BD, Sette AD, Sidney JC;
 DR WPI: 95-090681/12.
 DR Q85435.
 PR Human melanoma antigen. MAGE-1, Peptide(s) - useful for
 PT stimulating immune response against melanoma
 PS Example 1; Fig 1; 59pp; English.
 CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
 CC to produce the C-terminal MAGE-1 peptides described in R70915 to
 CC R70699. These peptides are useful for defining epitopes that
 CC engender a HLA-restricted cytotoxic lymphocyte activity against
 CC MAGE-1 antigens. Compns. containing these peptides can be
 CC administered, as a vaccine to patients susceptible to MAGE
 CC associated tumours, e.g. melanomas.
 Sequence 309 AA;

Query Match Score 52; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.016e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EADPTGHSY 9
 |||||
 Db 161 EADPTGHSY 169

RESULT 8
 R65112 ID R65112 standard; peptide; 9 AA.
 AC R65112.
 DR 06-OCT-1995 (first entry)
 DE MAGE 1 immunogenic peptide 161-169.
 KW MAGE 1; immunogenic peptide 161-169; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.
 PN WO9504817-A.
 PD 16-FEB-1995.
 PR 01-AUG-1994; U08672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Celis E., Kubo R., Serra H., Tsai V., Wentworth P;
 DR WPI: 95-090895/12.
 PT In vitro activation of cytotoxic T cells for selected killing of
 PT target cells - for treating e.g. cancer, AIDS, hepatitis etc. by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide
 PS Example 3; Page 35; 53pp; English.
 CC R65109-R65115 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 SQ Sequence 9 AA;

Query Match Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 9
 R75954 ID R75954 standard; Peptide; 9 AA.
 AC R75954.
 DR 06-MAR-1996 (first entry)
 DE Melanoma antigen (MAGE-1) epitope.
 KW MAGE-3; melanoma antigen; vaccine; immune response; immunogenic peptide;
 KW cytotoxic T lymphocyte response; CTL; melanoma; breast cancer; antibody.
 OS Homo sapiens.
 PN WO9519783-AI..
 PD 27-JUL-1995.
 PR 25-JAN-1994; U01000.
 PA (CYTE-) CYTEL CORP.
 PI Celis E., Grey HM, Rubo RT, Sette A;
 DR WPI: 95-269270/25.
 PT Immunogenic peptide(s) that induce immune response to cancer cells
 PT - that express a MAGE-3 protein peptide epitope used in vaccines or
 PT adoptive immuno-therapy to induce cytotoxic T lymphocytes
 PS Example; Page 33; 44pp; English.
 CC R75954 is derived from MAGE-1 protein. It was used to show the
 CC specificity of CTL response to MAGE-3 peptides shown in R75942-53.
 CC R75942 is derived from the sequence of the melanoma antigen (MAGE-3)
 CC protein and can be used to elicit a primary cytotoxic T lymphocyte
 CC response against cells expressing MAGE-3. Synthetic peptides R75945-53
 CC can be used therapeutically to elicit CTL responses to melanoma, breast,
 CC colon, prostate, or other cells which express proteins with this epitope.
 .CC The peptides have specific HLA-A1 binding capacity.
 SQ Sequence 9 AA;

Query Match Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC R82988; ID R82988 standard; Peptide; 9 AA.
 DT 26-FEB-1996 (first entry)
 DE P815 antigenic peptide.
 KW P815 antigen; PIA antigen; cancer; vaccine; vaccine.
 OS Synthetic.
 PN WO9523874-A1.
 PD 08-SEP-1995.
 PF 23-FEB-1995; U02203.
 PR 01-MAR-1994; US-204727.
 PR 10-MAR-1994; US-209172.
 PR 01-SEP-1994; US-299849.
 PA (LUDWIG) LUDWIG INST CANCER RES.
 PI Boon-Faillieu T, Brousse F, Chomez P, De Plaein E;
 De Smet C, Gaugier B, Lethe B, Marchand M, Patard J;
 PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
 DR WPI: 95-32058674/1.
 PT Determin of cancerous condition(s) - using a nucleic acid as a
 primer to determine expression of a MAGE tumour rejection antigen
 precursor
 PS Example 13: Page 22; 121pp; English.
 CC Using the sequence of the P815A antigen precursor gene P1A
 (T0176), an antigenic peptide (R82988) which was A+B+ (i.e.
 characteristic of cells which express both A and B antigens) was
 produced. The peptide lysed PO-HTR cells in the presence of
 cytolytic T lymphocyte cell lines, and may be useful as a vaccine
 component.
 SQ Sequence 9 AA;

RESULT 10
 R82988
 ID R82988 standard; Peptide; 9 AA.
 AC R82988; ID R82988 standard; Peptide; 9 AA.
 DT 26-FEB-1996 (first entry)
 DE P815 antigenic peptide.
 KW P815 antigen; PIA antigen; cancer; vaccine; vaccine.
 OS Synthetic.
 PN WO9523874-A1.
 PD 08-SEP-1995; U02203.
 PR 01-MAR-1994; US-204727.
 PR 10-MAR-1994; US-209172.
 PR 01-SEP-1994; US-299849.
 PA (LUDWIG) LUDWIG INST CANCER RES.
 PI Boon-faillieu T, Chen Y, Gatin-chesa P, Old LJ, Rettig WJ;
 PI Stockert E, Van der Bruggen P;
 DR WPI: 95-283605/37.
 PT New monoclonal antibody binding specifically to MAGE-1 - useful for
 diagnosis and monitoring of cancer, also new hybridomas, recombinant
 PT MAGE-1 and immunogenic peptide(s).
 PS Claim 12; Page 20; 33pp; English.
 CC A monoclonal antibody directed against the tumour rejection antigen
 (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HBB11540. The monoclonal antibody is
 specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antisera.
 SQ Sequence 12 AA;

Query Match Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC R78824; ID R78824 standard; peptide; 9 AA.
 DT 26-MAR-1996 (first entry)
 DE MAGE-1; cytotoxic T lymphocyte epitope.
 KW MAGE-1; cytotoxic T; CTL; epitope; helper T; HTL; lymphocyte;
 KW cell; viruses; parasites; tumours; antigens; disease prevention;
 KW treatment.
 Homo sapiens.
 PN WO9522317-A1.
 PD 24-AUG-1995.
 PR 16-FEB-1994; US-197484.
 PA (CYTE-) CYTEL CORP.
 PI Celis E, Chestnut RW, Grey H, Sette AD, Vitiello MA;
 DR WPI: 95-302545/39.
 PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 PT bacterial, parasitic or tumour antigens - useful in the treatment
 PT and prevention of diseases associated with the antigen e.g.
 PT hepatitis B
 PS Disclosure; Page 17; 109pp; English.

RESULT 11
 R78824
 ID R78824 standard; peptide; 9 AA.
 AC R78824; ID R78824 standard; peptide; 9 AA.
 DT 05-FEB-1996 (first entry)
 DE MHC class I restricted antigenic peptide #2.
 KW MHC class I; antigen; MAGE; melanoma; breast; cancer; bladder cancer;
 KW parasite; human; animal.
 OS Synthetic.
 PN WO928958-A1.
 PD 02-NOV-1995.

Query Match Score 52; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC R83932; ID R83932;
 DT 05-FEB-1996 (first entry)
 DE MHC class I restricted antigenic peptide #2.
 KW MHC class I; antigen; MAGE; melanoma; breast; cancer; bladder cancer;
 KW parasite; human; animal.
 OS Synthetic.
 PN WO928958-A1.

PF 21-APR-1995; U04975.
 PR 22-APR-1994; US-233496.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PI Dyall R, Nikolic-Zugovic J;
 DR WPI: 95-38288/49.
 Cytoxic T-cell induction by MHC class I-restricted Peptide in
 adjuvant - useful for treating tumours and bacterial or parasitic
 pathogenic diseases
 PT Claim 11; Page 38; 50PP; English.
 The sequences given in R83931-49 are MHC class I restricted 8-12
 amino acid antigenic peptides. This peptide is derived from MAGE
 and is present in melanoma, breast and bladder cancer. These
 peptides may be administered to a subject in combination with a
 suitable adjuvant, pref. Titermax (RTM), to induce cytotoxic T-
 lymphocytes. This method may be used in the treatment of a tumour
 or a pathogenic disease, esp. diseases of bacterial or parasitic
 origin, in humans and animals, e.g. monkeys, dogs cows, horses, etc.
 Sequence 9 AA;

CC Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 Db 1 EADPTGHSY 9

RESULT 14
 R90692 standard; peptide; 9 AA.
 ID R90692;
 AC R90692;
 DT 31-JUL-1996 (first entry)
 DE Human leukocyte antigen (HLA-A1) presented peptide MZ2-E.
 KW Human leukocyte antigen; HLA-A1; MAGE-1 derived;
 blood mononuclear cell; BMC; CD8-beta+ cell; cytolytic T cell;
 CTL cell; treatment; tumour cell; diagnosis; assay;
 presented peptide.
 OS Synthetic.
 PN W09535500-A1.
 PD 28-DEC-1995.
 PF 14-JUN-1995; U07559.
 PR 17-JUN-1994; US-261541.
 PA (LUDW) LUDWIG INST CANCER RES.
 PI Boon Falleur T, Coulie P, van Der Bruggen P;
 DR WPI: 96-058510/06.
 Prod'n of specific cytolytic T cell sub-populations - by contacting
 blood mononuclear cells with specific peptide(s) and a population of
 CD8-beta(+) cells
 PS Claim 5; Page 19; 25pp; English.
 The present peptide is the human leukocyte antigen (HLA-A1), MAGE-1-
 derived presented peptide, MZ2-E. By contacting a sample of blood
 mononuclear cells (BMC) with the peptide (which binds directly to
 HLA-A1 mois. on the surface of the BMC) and CD8-beta+ cells (which
 stimulate peptide/HLA-A1 complex specific CD8-beta+ cells), a
 subpopulation can be obt'd. The CTL cells obt'd. can be
 administered to a patient to treat tumour cell related conditions,
 and can be used in diagnostic methods, e.g. in assays for the
 peptide/HLA-A1 complex.
 Sequence 9 AA;

CC Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 Db 1 EADPTGHSY 9

Query Match Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EADPTGHSY 9
 Db 1 EADPTGHSY 9

Search completed: December 10, 1999, 14:27:26
 Job time: 11234 sec

Query Match Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EADPTGHSY 9
 Db 1 EADPTGHSY 9

RESULT 3
 138668 MAGE-9 antigen - human
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 04-Sep-1998
 R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br
 on, T.
 Immunogenetics 40, 360-369, 1994
 A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
 A;Reference number: 138659; MUID:95012457
 A;Accession: I38668
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-315 <RES>
 A;Cross-references: EMBL:U10694; NID:9533527; PID:9533528
 C;Genetics:
 A;Gene: GDB:MAGEA9; MAGE9
 A;Cross-references: GDB:331125
 A;Map position: Xp21.3-Xp21.3
 A;Introns: #status absent
 C;Superfamily: tumor associated protein MAGE

Query Match Score 43; DB 2; Length 315;
 Best Local Similarity 77.8%; Pred. No. 0.6%;
 Matches 0; Indels 2; Gaps 0;
 RESULT 6
 RGASWA
 regulatory protein wetA - Emeritella nidulans
 C;Species: Emeritella nidulans, Aspergillus nidulans
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Oct-1997
 C;Accession: A39665
 R;Marshall, M.A.; Timberlake, W.E.
 Mol. Cell. Biol. 11, 55-62, 1991
 A;Title: Aspergillus nidulans wetA activates spore-specific gene expression.
 A;Reference number: A39665; MUID:91094871
 A;Molecule type: DNA
 A;Residues: 1-555 <MR>
 A;Cross-references: GB:M60528; GB:M35758; NID:g168108; PID:g168109
 C;Comment: The products of the genes brA, abAA, and wetA are required for activation
 C;Genetics:
 C;Superfamily: regulatory protein wetA
 C;Keywords: transcription regulation

RESULT 4
 138667 MAGE-8 antigen - human
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 04-Sep-1998
 R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br
 on, T.
 Immunogenetics 40, 360-369, 1994
 A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
 A;Reference number: 138659; MUID:95012457
 A;Accession: I38667
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-234 <RES>
 A;Cross-references: EMBL:U10693; NID:9533525; PID:9533526
 C;Genetics:
 A;Gene: GDB:MAGE8; MAGE8
 A;Cross-references: GDB:331123
 A;Map position: Xq28-Xq28
 A;Introns: #status absent
 C;Superfamily: tumor associated protein MAGE

Query Match Score 43; DB 2; Length 234;
 Best Local Similarity 77.8%; Pred. No. 0.44%;
 Matches 0; Indels 2; Gaps 0;
 RESULT 7
 A42551 genome polyprotein - dengue virus type 1 (strain Singapore S275/90)
 N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein
 a; nonstructural protein NS4b; nonstructural protein NS5
 C;Species: dengue virus type 1
 C;Accession: A42551
 R;Fu, J.; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.
 Virology 198, 933-958, 1992
 A;Title: Full-length cDNA sequence of dengue type 1 virus (Singapore strain S275/90).
 A;Reference number: A42551; MUID:92263809
 A;Accession: A42551
 A;Molecule type: genomic RNA
 A;Residues: 1-396 <PU>
 A;Cross-references: GB:M87512
 C;Superfamily: yellow fever virus genome polyprotein; DEAD/H box helicase homology

RESULT 5
 138660 MAGE-11 antigen - human
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 04-Sep-1998
 R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br

C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 FF:1-114/Product: capsid protein #status predicted <CAP>
 FF:115-211/Product: membrane protein precursor #status predicted <MEP>
 FF:115-214/Domain: nonterminal signal sequence #status predicted <SIG>
 FF:267-279/Domain: membrane protein #status predicted <MEM>
 FF:282-714/Domain: transmembrane #status predicted <TM>
 FF:715-1114/Product: envelope protein #status predicted <ENV>
 FF:718-1344/Product: nonstructural protein NS1 #status predicted <NS1>
 FF:118-1344/Domain: nonstructural protein NS2a #status predicted <NS2a>
 FF:1475-2093/Product: nonstructural protein NS2b #status predicted <NS2b>
 FF:1668-1938/Domain: DEAD/H box helicase homology #DEAD>
 FF:1668-1675/Region: nucleotide-binding motif A (P-loop)
 FF:1755-1760/Region: nucleotide-binding motif B
 FF:1759-1762/Region: DEAH motif
 FF:2094-2243/Product: nonstructural protein NS4a #status predicted <NS4a>
 FF:2244-4492/Product: nonstructural protein NS4b #status predicted <NS4b>
 FF:2493-3396/Product: nonstructural protein NS5 #status predicted <NS5>
 FF:183-347/433/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.2%; Score 36; DB 1; Length 3396;
 Best Local Similarity 75.0%; Pred. No. 1.6e-02; Mismatches 1; Indels 0; Gaps 0;

Qy	1 EADPTGHS 8
D _b	3383 ESDPKGHS 3390

RESULT 8

JC2361

tumor-associated antigen MAGE-3 - human

N Alternative names: MAGE 3 protein

C Species: Homo sapiens (man)

C Accession: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998

C Accession: JC2361; PH1296; I138138

R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 20., 549-555, 1994

A:Title: Cloning and analysis of MAGE-1-related genes .

A:Reference number: JC2358; MUID:94311935

A:Accession: JC2361

A:Molecule type: mRNA

A:Residue 1-314 <DIN>

A:Experimental source: melanoma cell line DM150

A:Residue 1-168 <TRA>

A:Residues: 1-314 <RES>

A:Residues: 1-168 <TRA>

A:Residues: 1-314 <RES>

A:Cross references: EMBL:U03735; NID:9468825; PID:q468826

C:Superfamily: tumor associated protein MAGE

C:Genes:

A:Gene: MAGE-3

F:168-116/Region: HLA-A1 binding #status predicted

Query Match 69.2%; Score 36; DB 2; Length 314;

Best Local Similarity 66.7%; Pred. No. 1.3e-02; Mismatches 0; Indels 0; Gaps 0;

Qy	1 EADPTGHSY 8
D _b	3383 ESDPKGHS 3390

A; Accession: PH1299
A; Molecule type: DNA
A; Residues: 1-9 <TRA>
A; Accession: PH1300
A; Molecule type: DNA
A; Residues: 1-9 <TR2>

Query Match 69.2%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; #text_change 09-Sep-1997

Db 374 EPDSSGHSY 382
RESULT 12
S02168 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoRI124/3 chain hsdr - Escherichia coli
C; Alternate names: type I restriction enzyme EcoRI124/3 Chain hsdr
C; Species: Escherichia coli
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Sep-1997
C; Accession: S02168
R; Price, C.; Lingner, J.; Bickle, T.A.
J. Mol. Biol. 205, 115-125, 1989
A; Title: Basis for changes in DNA recognition by the EcoRI124 and EcoRI124/3 type I DNA
A; Reference number: S02166; MUID:89178638
A; Cross-references: EMBL:X13145; NID:g388978; PID:941750
A; Gene: hsdr
A; Genome: plasmid
C; Keywords: DNA binding; hydrolase

Qy 1 EADPFGHSY 9
Db 1 EADPFSNTY 9
A; Accession: S02168
A; Molecule type: DNA
A; Residues: 1-1033 <PR1>
C; Genetics:

A39216 plasma cell membrane glycoprotein PC-1 - human
N; Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C; Species: Homo sapiens (man)
C; Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 29-Aug-1997
C; Accession: S21016; S23587; S51030
R; Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Garson, O.M.; Goding, J.W.
J. Biol. Chem. 265, 17506-17511, 1990
A; Reference number: A39216; MUID:91009202
A; Accession: A39216
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-95 <BUC>
A; Cross-references: GB:J05654
R; Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; Suzuki, T.;
Arch. Biochem. Biophys. 295, 180-187, 1992
A; Molecular cloning of cDNAs for human fibroblast pyrophosphatase.
A; Reference number: S21706; MUID:92246539
A; Accession: S21706
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-95 <FUN1>
A; Accession: S23587
A; Molecule type: protein
A; Residues: 116-121-247-271, 'X', 273-275-279-280, 'X', 282-283-303-316; 362-364; 449-465-482-
A; Note: it is uncertain whether Met-1 or Met-53 is the initiator
R; Belli, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A; Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline Phos.
A; Reference number: S51030
A; Accession: S51030
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-80 <BE1>
C; Genetics:
A; Gene: GDB:PDNP1; M6S1; NPPS
A; Cross-references: GDB:132615; OMIM:173335
A; Map position: 6q22-6q23
C; Superfamily: nucleotide pyrophosphatase: somatomedin B homology
C; Keywords: glycoprotein; phosphoric diester hydrolase; transmembrane protein
F; 7/7-7/Domain: transmembrane #status predicted <TMM>
F; 1/144/Domain: somatomedin B homology <SBH1>
F; 1/145-188/Domain: somatomedin B homology <SBH2>
F; 179-285, 341-477, 578, 585-643, 700-731, 748/Binding site: carbohydrate (Asn) (covalent) #
F; 254/Active site: Thr (covalent substrate-binding) #status predicted

Query Match 67.3%; Score 35; DB 2; Length 925;
Best Local Similarity 66.7%; Pred. No. 63; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2; #text_change 08-Feb-1995 #sequence_revision 20-Feb-1995
Qy 1 EADPFGHSY 9
Db 1 EADPFSNTY 9
A; Accession: S02168
A; Molecule type: DNA
A; Residues: 1-1033 <PR1>
C; Genetics:

S33938 penton protein (III) - human adenovirus 12
C; Species: Mastadenovirus h12 (human adenovirus 12)
C; Date: 20-Feb-1995 #sequence_revision 08-Sep-1997
C; Accession: S33938
R; Spengel, J.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID:38295937
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, D.; Garnier, T.; Connor, R.; Davies, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, P.; Rajandream, M.A.; Rutten, J.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sgatzes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: F0769 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C; Accession: F0769
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, D.; Garnier, T.; Connor, R.; Davies, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, P.; Rajandream, M.A.; Rutten, J.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sgatzes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: F0769 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
A; Accession: F0769
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-98 <CC1>
A; Cross-references: GB:Z73902; GB:AU123456; NID:g1261576; PID:e245016; PID:g1340088
A; Experiment source: strain H37Rv
C; Genetics:
A; Gene: Rv1322

Query Match 67.3%; Score 35; DB 2; Length 98;
Best Local Similarity 66.7%; Pred. No. 6.1; Indels 3; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; #text_change 08-Feb-1995 #sequence_revision 20-Feb-1995
Qy 1 EADPFGHSY 9
Db 24 EAGPDGHEY 32
A; Accession: S33938
A; Molecule type: DNA
A; Residues: 1-1033 <PR1>
C; Genetics:

RESULT 14

A; Reference number: S33928
 A; Accession: S33938
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-497 <SPR>
 A; Cross-references: EMBL:X73487; NID:9313361; PID:9313372
 C; Superfamily: adenovirus penton protein

Query Match 65.4%; Score 34; DB 2; Length 497;
 Best Local Similarity 66.7%; Pred. No. 51; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 3;

```
Qy  1 EADPTGHSY 9
  | | | | |
Db  310 ETDPKGRSY 318
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RESULT 15
 S49008
 fork head protein - African clawed frog
 C; Species: Xenopus laevis (African clawed frog)
 C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
 C; Accession: B56556
 R; Lef, J.; Clement, J.H.; Oschwald, R.; Koester, M.; Knoechel, W.
 Mech. Dev. 45, 117-126, 1994
 A; Title: Spatial and temporal transcription patterns of the forkhead related XFD-2/XFD-2
 A; Reference number: S49008; MUID:94257528
 A; Accession: S49008
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-370 <LEP>
 A; Cross-references: EMBL:X74315; NID:511159; PID:9511160

R; Knoechel, S.; Lef, J.; Clement, J.; Klocke, B.; Hille, S.; Koster, M.; Knoechel, W.
 Mech. Dev. 38, 157-165, 1992
 A; Title: Activin A induced expression of a fork head related gene in posterior chordames
 A; Reference number: A56556; MUID:93041288
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 118-228 <KN0>
 A; Experimental source: gastrula

A; Note: sequence extracted from NCBI backbone (NCBIP:118173)
 C; Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology
 F:127-218/Domain: fork head DNA binding domain homology <FHD>
 A; Cross-references: EMBL:X74315; NID:511159; PID:9511160

Query Match 65.4%; Score 34; DB 2; Length 370;
 Best Local Similarity 75.0%; Pred. No. 38; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 2;

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Qy  1 EADPTGHS 8
  | | | | |
Db  257 ELSPTGHS 264
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GenCore version 4.5
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OM protein - protein search, using sw mode1

Run on: December 8, 1999, 19:03:56 ; Search time 9.88 Seconds
(without alignments)
25.750 Million cell updates/sec

Title: US-08-B19-669D-26

Perfect score: 52 Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	52	100.0	309	1	MAG1_HUMAN	P43355	homo sapien
2	44	84.6	369	1	MAGA_HUMAN	P43363	homo sapien
3	43	82.7	234	1	MAG8_HUMAN	P43361	homo sapien
4	43	82.7	315	1	MAG9_HUMAN	P43362	homo sapien
5	42	80.8	319	1	MAGB_HUMAN	P43364	homo sapien
6	37	71.2	555	1	WETA_EMEINI	P22022	emericella
7	36	69.2	314	1	MAG3_HUMAN	P43357	homo sapien
8	36	69.2	314	1	MAG6_HUMAN	P43360	homo sapien
9	36	63.2	3396	1	POLG_DENIS	P33478	d genome po
10	35	67.3	346	1	MGB4_HUMAN	O15481	homo sapien
11	35	67.3	1033	1	PC1_HUMAN	P22413	homo sapien
12	35	67.3	1033	1	TIR1_ESCOLI	P10486	escherichia
13	35	67.3	98	1	Y037_BYCTU	Q10385	mycobacterium
14	34	65.4	497	1	PEN3_ADE12	P36716	human adeno
15	34	65.4	878	1	Y9X_YEAST	P74918	saccharomyces
16	33	63.5	1523	1	DPOL_THE9M	P56336	thermococcus
17	33	63.5	775	1	DPOL_THE99	P50400	cellulomonas
18	33	63.5	747	1	GUND_CELL1	P32874	saccharomyces
19	33	63.5	2273	1	HFA1_YEAST	P33417	saccharomyces
20	33	63.5	597	1	IXR1_YEAST	P20013	trametes ve
21	33	63.5	372	1	LIGC_FRAVE	P21139	rattus norv
22	33	63.5	1040	1	MAN1_RAT	P51387	homo sapien
23	33	63.5	488	1	SUOX_HUMAN	P07116	rattus norv
24	33	63.5	488	1	SUOX_RAT	P52638	borna disea
25	33	63.5	503	1	VP57_BDV	009165	mus musculu
26	32	61.5	399	1	CAQS_MOUSE	P07221	oryctolagus
27	32	61.5	395	1	CQS_RABIT	P39226	candida alb
28	32	61.5	416	1	CC3_CANAL	P51511	homo sapien
29	32	61.5	669	1	COGU_HUMAN	P98081	drosophila
30	32	61.5	2411	1	DAB_DROME	Q24314	drosophila
31	32	61.5	1002	1	DOR_DROME	P46211	aquifex pyr
32	32	61.5	700	1	EFG_AQUPY	P54382	bacillus su
33	32	61.5	283	1	FOLD_BACSU	Q91590	xenopus lae
34	32	61.5	1360	1	GLI1_XENLA	P11001	streptococc
35	32	61.5	1597	1	GTF1_STRDO	P27470	streptococc
36	32	61.5	1592	1	GTF2_STRDO	P05619	equus cabal
37	32	61.5	379	1	IIEU_HORSE	P13934	brassica na
38	32	61.5	280	1	LE76_BRANA	P43358	homo sapien
39	32	61.5	317	1	MAG4_HUMAN	P10456	klebsiella
40	32	61.5	349	1	NRLB_KLEPN	P55042	homo sapien
41	32	61.5	269	1	RAD_HUMAN	P55043	rattus norv
42	32	61.5	268	1	RAD_RAT	P33460	caprine art
43	32	61.5	133	1	REV_CAEVC		

ALIGNMENTS

44 32 61.5 640 1 TPB5_BPT5
45 32 61.5 689 1 YYAL_BACSU

P23207 bacterioph
P37512 bacillus su

RESULT 1	MAG1_HUMAN	STANDARD	PRT;	309 AA.
ID	P43355; 000345;			
AC	P43355;			
DT	01-NOV-1995 (REL. 32, CREATED)			
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN M22-E).			
GN	MAG1 OR MAGEL OR MAGE1A.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUOTHERIA; PRIMATES; CATARRHENI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 92083861.			
RA	VAN DER BRUGGEN P., TRAVERSARI C., CHOMEZ P., LURQUIN C., DE PLAEN E.,			
RA	VAN DEN BYNDE B., KNUTH A., BOON T.,			
RA	"A gene encoding an antigen recognized by cytolytic T lymphocytes on a human melanoma."			
RA	SCIENCE 254:1643-1647(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-SKIN;			
RX	MEDLINE; 94311935.			
RA	DING M., BECK R.J., KELLER C.J., FENTON R.G.;			
RA	"Cloning and analysis of MAGE-1-related genes."			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).			
RN	[3]			
RA	SEQUENCE FROM N.A.			
RA	GLOCKNER G., RUMP A., NORDSTEIK G., HINZMANN B., KIOSCHIS P., HEISS N., POUSTKA A., BAUER D., DRESCHER B., KNOB A.,			
RA	HEISS N., POUSTKA A., BAUER D., DRESCHER B., KNOB A., ROSENTHAL A.;			
RL	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDJB DATA BANKS.			
RN	[4]			
PP	MUTAGENESIS			
RC	TISSUE-BLOOD;			
RX	MEDLINE; 94157413.			
RA	GAUCIER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P., GAUDIO R.J., DE PLAEN E., LETHE B., BRASSER F., BOON T.;			
RA	"Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous cytolytic T lymphocytes."			
RT	J. EXP. MED. 179:91-93(1994).			
RL	-!- FUNCTION: NOT KNOWN. THOUGH MAY PLAY A ROLE IN EMBRYONAL DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLYTIC T LYMPHOCYTES.			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LONG CARCINOMA AND BREAST CARCINOMA. BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND LYMPHOMAS.			
CC	-!- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A POLYMORPHISM OF THE MAG-1 GENE.			
CC	-!- SIMILARITY: BELONGS TO THE MAGE FAMILY.			
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CC	-!- POLYMORPHISM: THE MAG-1 GENE.			
CC	-!- SIMILARITY: BELONGS TO THE MAGE FAMILY.			

FT VARIANT 32 32 T -> A
FT DOMAIN 33 36 POLY-SER.
FT MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.
FT CONFLICT 169 169 Y->A: ABOLISHES HLA-A1 BINDING.
FT SEQUENCE 72 72 R -> Q (IN REF. 3).
SQ 309 AA: .34342 MW: E6CB1300 CRC32;

Query Match 100.0%; Score 52; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0091; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EADPTGHSY 9
Db 161 EADPTGHSY 169

RESULT 2
MAGA_HUMAN STANDARD; PRT; 369 AA.
ID MAGA_HUMAN
AC P43363;
DT 01-NOV-1995 (REL: 32, CREATED)
DT 01-NOV-1995 (REL: 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL: 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 10 (MAGE-10 ANTIGEN).
GN MAGE10 OR MAGE10.
OS HOMO SAPIENS (HUMAN).
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
SEQUENCE FROM N.A.
MEDLINE; 95012457.
RN RP
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
SEQUENCE FROM N.A.
MEDLINE; 95012457.
RA DE PIAEN K., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEW W., BOON T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family";
RL IMMUNOGENTICS 40:360-369(1994).
-!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
PROGRESSION.
-!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
FOR TESTES AND PLACENTA.

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
CC
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or send an email to license@isb-sib.ch).

CC
CC DR U10693; G533526; -
CC KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
CC DOMAIN 40 43 POLY-SER.
CC SEQUENCE 234 AA: 25197 MW: D491BC3 CRC32;

Query Match 82.7%; Score 43; DB 1; Length 234;
Best Local Similarity 77.3%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9.
Db 171 EVDPAGHSY 179

RESULT 4
MAG9_HUMAN STANDARD; PRT; 315 AA.
ID MAG9_HUMAN
AC P43365; Q92910.
DT 01-NOV-1995 (REL: 32, CREATED)
DT 01-NOV-1997 (REL: 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 9 (MAGE-9 ANTIGEN).
GN MAGE9 OR MAGE9.
OS HOMO SAPIENS (HUMAN).
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
SEQUENCE FROM N.A.
MEDLINE; 95012457.
RA DE PIAEN K., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEW W., BOON T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family";
RL IMMUNOGENTICS 40:360-369(1994).
[2]
RN SEQUENCE FROM N.A.
RA TIMMS K.M., BONDESON M.L., ANSARI-LARI M.A., LAGERSTEDT K.,

Query Match 84.6%; Score 44; DB 1; Length 369;
Best Local Similarity 77.8%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 1;

Qy 1 EADPTGHSY 9
Db 193 EVDPAGHSF 201

RESULT 3
MAG8_HUMAN STANDARD; PRT; 234 AA.
ID MAG8_HUMAN
AC P43361;

RA NELSON D.L.; PETTERSSON U.; GIBBS R.A.; EMBL/GENBANK/DDBJ DATA BANKS.
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 PROGRESSION.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 FOR TESTES AND PLACENTA.
 CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

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CC DR EMBL; U10686; G533513; KW MULTIGENE; TUMOR ANTIGEN.
 SQ SEQUENCE 319 AA; 35536 MW; E3DBDEF CRC32;

Query Match 80.8%; Score 42; DB 1; Length 319;
 Best Local Similarity 77.8%; Pred. No. 0.73; Mismatches 2; Indels 0; Gaps 0;

CC RESULT 6
 WETA_ELEMENI PRT; 555 AA.
 ID WETA_ELEMENI STANDARD; PRT;
 AC P22022; DT 01-AUG-1991 (REL. 19, CREATED)
 DR 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE REGULATORY PROTEIN WETA.
 GN WETA.
 OS EMERICELLA NIJULANS (ASPERGILLUS NIJULANS).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; EUASCOMYCETES; PLECTOMYCETES;
 OC EUROTIALES; TRICHOCLADACEAE; EMERICELLA.
 RN [1] OC
 RP SEQUENCE FROM N.A.
 RX MARSHALL M.A.; TIMBERLAKE W.E.;
 RA "Aspergillus nidulans weta activates spore-specific gene expression.";
 RT MOL. CELL. BIOL. 11:155-62(1991).
 CC -!- FUNCTION: RESPONSIBLE FOR ACTIVATING A SET OF GENES WHOSE PRODUCTS
 MAKE UP THE FINAL TWO CONIDIAL WALL LAYERS OR DIRECT THEIR
 ASSEMBLY AND THOUGH THIS ACTIVITY IS RESPONSIBLE FOR ACQUISITION
 OF SPORE DORMANCY.
 CC -!- FUNCTION: BRLA, ABAA & WETA ARE PIVOTAL REGULATORS OF CONIDIOPHORE
 DEVELOPMENT AND CONIDIUM MATURATION. THEY ACT INDIVIDUALLY AND
 TOGETHER TO REGULATE THEIR OWN EXPRESSION AND THAT OF NUMEROUS
 OTHER SPORULATION-SPECIFIC GENES.
 CC -!- DEVELOPMENTAL STAGE: THE WETA GENE IS ACTIVATED ONLY DURING
 CONIDIOPHORE DEVELOPMENT, AND ITS mRNA ACCUMULATES PREFERENTIALLY
 IN MATURE CONIDIUM.
 CC -!- DOMAIN: HAS AN ACIDIC N-TERMINUS (AA 1-52) FOLLOWED BY A SER-,
 THR-, PRO-RICH DOMAIN (AA 125-233) AND A BASIC C-TERMINUS (AA
 461-555).
 CC -!- SIMILARITY: TO P.CHRYSONOGENUM WETA.

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CC DR EMBL; M60528; G168109; DR PIR; A39665; RGASWA;
 KW DEVELOPMENTAL PROTEIN; CONIDIATION; TRANSCRIPTION REGULATION;
 SQ SEQUENCE 555 AA; 60275 MW; 5BAF6B20 CRC32;

Query Match 71.2%; Score 37; DB 1; Length 555;
 Best Local Similarity 87.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

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RESULT 7
MAGE3_HUMAN STANDARD; PRT; 314 AA.

AC P43357; ID HUMAN ;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1997 (REL. 32, LAST SEQUENCE UPDATE)
 DE MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN) (ANTIGEN M22-D).
 GN MAGE3 OR MAGE3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 TISSUE-BLOOD:
 RX MEDLINE: 94157413.
 RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
 RA GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
 RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
 autologous cytolytic T lymphocytes.";
 RT J. EXP. MED. 179:921-930(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 TISSUE-SKIN:
 RX MEDLINE: 94311935.
 RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
 RT "Cloning and analysis of MAGE-1-related genes.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
 CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR
 DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
 CYTOLYTIC T LYMPHOCYTES.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
 LEUKEMIAS AND LYMPHOMAS.
 CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
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 or send an email to license@ebi.sib.ch).
 CC DR U03755; G468826; -.
 CC KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
 CC FT DOMAIN 40 43 POLY-SER.
 DR EMBL; U03755; G468826; -.
 CC KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
 CC FT DOMAIN 170 170 D->A: ABOLISHES HLA-A1 BINDING.
 DR FT MUTAGEN 176 176 Y->A: ABOLISHES HLA-A1 BINDING.
 SQ SEQUENCE 314 AA; 34747 MW; AC557A64 CRC32;

Query Match 69.2%; Score 36; DB 1; Length 314;
 Best Local Similarity 66.7%; Pred. No. 9.8%;
 Matches 0; Mismatches 3; Indels 0; Gaps 0;
 Db 168 EVDPIGHVY 176

RESULT 8
MAGE6_HUMAN STANDARD; PRT; 314 AA.

AC P43360; ID HUMAN ;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1997 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MELANOMA-ASSOCIATED ANTIGEN 6 (MAGE-6 ANTIGEN) (MAGE3B).
 GN MAGEA6 OR MAGE6.

Query 1 EADPTGHSY 9
 | | | | |
 168 EVDPIGHVY 176

Query Match 69.2%; Score 36; DB 1; Length 314;
 Best Local Similarity 66.7%; Pred. No. 9.8%;
 Matches 0; Mismatches 3; Indels 0; Gaps 0;
 Db 168 EVDPIGHVY 176

RESULT 9
POLG_DEN1S STANDARD; PRT; 3396 AA.

AC P33478; ID POLG_DEN1S ;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
 PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN C (CORE PROTEIN); MATRIX
 PROTEINS NS1, NS2A, NS2B, NS3A AND NS4B; HELICASE (NS3); RNA-DIRECTED
 RNA POLYMERASE (EC 2.7.7.48) (NS5)).
 DE DENGUE VIRUS TYPE 1 (STRAIN SINGAPORE S275/S0).
 OS VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;

OC FLAVIVIRUS.
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE; 92263809.
 RA FU J., TAN B.H., YAP E.H., CHAN Y.C., TAN Y.H.;
 "Full-length cDNA sequence of dengue type 1 virus (Singapore strain
 S75/90)." Virology 188:953-958(1992).
 RL SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF THREE PROTEINS:
 CC PROTEIN PRM, PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A
 CC COMPLEX OF PROTEIN C AND MRNA.
 CC
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 CC
 EMBL: M87512; -; NOT_ANNOTATED_CDS.
 PIR: A42551; A42551.
 DR PF00869; Flavi_glycoprot; 1.
 DR PFAM; PF00948; Flavi_NS1; 1.
 DR PFAM; PF00949; Flavi_helicase; 1.
 DR PFAM; PF00952; Flavi_NS5; 1.
 DR PFAM; PF01002; Flavi_NS2B; 1.
 DR PFAM; PF01003; Flavi_capsid; 1.
 DR PFAM; PF01004; Flavi_M; 1.
 DR PFAM; PF01005; Flavi_NS2A; 1.
 DR HSSP; P14336; 1SVB.
 KW POLYPROTEIN; GLYCOPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE;
 KW CORE PROTEIN; COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING;
 KW TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.
 FT CHAIN 1 114 CAPSID PROTEIN C (POTENTIAL).
 FT PROPEP 115 205
 FT CHAIN 206 280
 FT CHAIN 281 774 ENVELOPE GLYCOPROTEIN M (POTENTIAL).
 FT CHAIN 775 1127 MAJOR ENVELOPE PROTEIN E (POTENTIAL).
 FT CHAIN 1128 1344 NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).
 FT CHAIN 1345 1474 NONSTRUCTURAL PROTEIN NS2A (POTENTIAL).
 FT CHAIN 1475 2093 NONSTRUCTURAL PROTEIN NS2B (POTENTIAL).
 FT CHAIN 2094 2243 HELICASE (NS).
 FT CHAIN 2244 2492 NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
 FT CHAIN 2493 3396 RNA-DIRECTED RNA POLYMERASE (NS5) (POTENTIAL).
 FT NP_BIND 1668 1675 ATP (POTENTIAL).
 FT SITE 1759 1762 DEAH BOX.
 FT TRANSMEM 267 279 POTENTIAL.
 FT TRANSMEM 753 769 POTENTIAL.
 FT DISULFID 283 310 BY SIMILARITY.
 FT DISULFID 340 396 BY SIMILARITY.
 FT DISULFID 354 385 BY SIMILARITY.
 FT DISULFID 372 401 BY SIMILARITY.
 FT DISULFID 465 565 BY SIMILARITY.
 FT DISULFID 582 613 BY SIMILARITY.
 FT CARBOHYD 183 183 POTENTIAL.
 FT CARBOHYD 347 347 BY SIMILARITY.
 FT CARBOHYD 433 433 POTENTIAL.
 SQ SEQUENCE 3396 AA; 379558 MW; F538880D CRC32;

Query Match Score 36; DB 1; Length 3396;
 Best Local Similarity Pred. No. 1.2e+02;
 Matches 1; Conservative 1; Indels 0; Gaps 0;

Qy 1 EADPTGHS 8
 Db 3383 ESSPKGHS 3390

RESULT 11
 PCL_HUMAN STANDARD; PRT; 873 AA.

Qy 1 EADPTGHS 9
 Db 168 EVNPTTISV 176

Query Match Score 67.3%; DB 1; Length 346;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHS 9
 Db 168 EVNPTTISV 176

Query Match Score 67.3%; DB 1; Length 346;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHS 9
 Db 168 EVNPTTISV 176

RESULT 11
 PCL_HUMAN STANDARD; PRT; 873 AA.

Qy 1 EADPTGHS 8
 Db 168 EVNPTTISV 176

Query Match Score 69.2%; DB 1; Length 3396;
 Best Local Similarity Pred. No. 1.2e+02;
 Matches 1; Conservative 1; Indels 1; Gaps 0;

Qy 1 EADPTGHS 8
 Db 3383 ESSPKGHS 3390

RESULT 10

RX MEDLINE; 91009202.
 RA BUCKLEY M.F., LOVELAND K.A., MCKINSTRY W.J., GARDON O.M., CODING J.W.;
 RT "Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human
 molecule, amino acid sequence, and chromosomal location.";
 RL J. BIOL. CHEM. 265:17506-17511(1990).
 [2]

RN SEQUENCE FROM N.A.
 RX MEDLINE; 92246539.
 RA FUNAKOSHI I., KATO H., HORIE K., YANO T., HORI Y., KOBAYASHI H.,
 INOUE T., SUZUKI H., FUKUI S., TSUKAHARA M., KAJII T.,
 YAMASHINA I.;
 RT "Molecular cloning of cDNAs for human fibroblast nucleotide
 pyrophosphatase.";
 RL ARCH. BIOCHEM. BIOPHYS. 295:180-187(1992).

CC -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOYLLATION.
 CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY TERMINATED
 CC OLIGO-NUCLEOTIDES.

CC -!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H₂O = 2 MONONUCLEOTIDE.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
 CC OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
 CC OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.

CC -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

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DR M57736; G189530; -.

DR EMBL; D12485; G219945; -.

DR EMBL; D12485; G219944; ALT_INIT.

DR PIR; A39216; A39216.

DR MIM; 173335; -.

DR PROSITE; PS00574; SOMATOMEDIN_B; 2.

DR PFAM; PF01033; Somatomedin_B; 2.

DR GLYCOPROTEIN; TRANSMEMBRANE; DUPLICATION; SIGNAL-ANCHOR; HYDROLASE.

FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN).

FT DOMAIN 46 873 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.

FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.

FT CARBOHYD 127 127 POTENTIAL.

FT CARBOHYD 233 233 POTENTIAL.

FT CARBOHYD 289 289 POTENTIAL.

FT CARBOHYD 425 425 POTENTIAL.

FT CARBOHYD 533 533 POTENTIAL.

FT CARBOHYD 591 591 POTENTIAL.

FT CARBOHYD 648 648 POTENTIAL.

FT CARBOHYD 679 679 POTENTIAL.

FT CARBOHYD 696 696 POTENTIAL.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

RESULT 13

Y037_MYCTU STANDARD;

ID Y037_MYCTU

AC Q1035;

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

GN MTCT10.07.

OS MYCOBACTERIUM TUBERCULOSIS.

OC BACTERIA; FIRACUTUS; ACTINOBACTERIA; ACTINOMYCETES; CORYNEBACTERIA; MYCOBACTERIUM.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RA MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;

RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

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DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE TYPE I RESTRICTION ENZYME ECOR124I R PROTEIN (EC 3.1.21.3).
 GN HSDR OR HSR.
 OS ESCHERICHIA COLI.

[2]

RN PLASMID INCIPIT R124/3.

OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAE;

OC ESCHERICHIA.

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE; 8917628.

RX PRICE C., LINGER J., BICKLE J., FIRMAN T.A., GLOVER S.W.;

RA "Basis for changes in DNA recognition by the EcoR124 and EcoR124/3

RT type I DNA restriction and modification enzymes.";

RL J. MOL. BIOL. 205:115-125 (1989).

CC -!- FUNCTION: THE ECOR124/3 I ENZYME RECOGNIZES 5'GAA(N7)TCG.

CC -!- SUBUNIT R IS REQUIRED FOR BOTH NUCLEASE AND ATPASE

CC ACTIVITIES, BUT NOT FOR MODIFICATION

CC -!- SUBUNIT: THE TYPE I RESTRICTION & MODIFICATION SYSTEM IS COMPOSED

CC OF THREE POLYPEPTIDES R, M AND S.

CC -!- TYPE I RESTRICTION AND MODIFICATION ENZYMES ARE COMPLEX, MULTI-

CC FUNCTIONAL SYSTEMS WHICH REQUIRE ATP, S-ADENOSYL METHIONINE AND

CC MG (2+) AS CO-FACTORS AND, IN ADDITION TO THEIR ENDONUCLEOLYTIC

CC AND METHYLASE ACTIVITIES, ARE POTENT DNA-DEPENDENT ATPASES.

CC -!- SIMILARITY: WITH ATPases.

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CC

DR EMBL; X13145; G41750; -.

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 1033 AA; 119656 MW; 9E988CC1 CRC32;

Query Match Best Local Similarity 67.3%; Score 35; DB 1; Length 1033;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 1033 AA; 119656 MW; 9E988CC1 CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 1033;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 1033 AA; 119656 MW; 9E988CC1 CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB 1; Length 873;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

DR PIR; S02168; S02168.

DR PR00748; ECOR124I.

DR PLASMID; RESTRICTION SYSTEM; HYDROLASE; DNA-BINDING; ATP-BINDING.

SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match Best Local Similarity 66.7%; Score 35; DB

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CC or send an email to license@isb-sib.ch).

CC EMBL: Z73502; E245016; -.

CC HYPOTHETICAL PROTEIN.

CC SEQUENCE 98 AA; 11334 MW; 8E3C8C75 CRC32;

Query Match 67.3%; Score 35; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 4.5.;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EADPFGHSY 9

| | | | |

Db 24 EADPGDHEY 32

RESULT 14
PEN3_ADE12 STANDARD; PRT; 497 AA.
ID PEN3_ADE12 STANDARD; PRT; 497 AA.

AC P36716; -.

CC DT 01-JUN-1994 (REL. 29, CREATED)

CC DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)

CC DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

CC DE PENTON PROTEIN (VIRION COMPONENT III) (PENTON BASE PROTEIN).

CC PIII

CC HUMAN ADENOVIRUS TYPE 12.

CC OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE; MASTADENOVIRUS.

CC RN [1]

CC RP SEQUENCE FROM N.A.

CC RX MEDLINE; 94076430.

CC RA SPRENGEL, J., SCHMITZ, B., HEUSS-NEITZEL, D., ZOCK, C., DOERFLER, W.: "Nucleotide sequence of human adenovirus type 12 DNA: Comparative functional analysis." J. VIROL. 68:3779-3809(1994).

CC J. VIROL. 68:3779-3809(1994).

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CC DR EMBL; X73487; G313372; -.

CC DR PIR; S33938; S33938.

CC KW LATE PROTEIN.

CC SQ SEQUENCE 497 AA; 56393 MW; ASBEC571 CRC32;

Query Match 65.4%; Score 34; DB 1; Length 497;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EADPFGHSY 9

| | | | |

Db 310 EADPKGRSY 318

RESULT 15
YB9X_YEAST STANDARD; PRT; 878 AA.
ID YB9X_YEAST STANDARD; PRT; 878 AA.

AC P38119; -.

CC DT 01-OCT-1994 (REL. 30, CREATED)

CC DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)

CC DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

CC DE HYPOTHETICAL 98.1 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PAF1-MRPL27

CC INTERGENIC REGION.

CC YBR281C OR YBR018.

CC SACCHAROMYCETES CERESIAE (BAKER'S YEAST).

CC EUKARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;

CC SACCHAROMYCETACEAE; SACCHAROMYCETES.

CC [1]

RP SEQUENCE FROM N.A.
RC STRAIN=S288C;

RC MEDLINE; 9437872.

RC HOLMSTROM K., BRANDT T., KALLESOE T.;

CC "The sequence of a 32,420 bp segment located on the right arm of

CC chromosome II from Saccharomyces cereisiae.";

CC !- SIMILARITY: CONTAINS ? WD REPEATS (TRP-ASP DOMAINS).

CC -----

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CC -----

CC DR EMBL; Y76053; G429126; -.

CC DR EMBL; Z36150; G536726; -.

CC DR PIR; S44543; S44543.

CC DR PIR; S39137; S39137.

CC DR PROSITE; PS00578; WD_REPEATS; 2.

CC KW HYPOTHETICAL PROTEIN; REPEAT; WD_REPEATS

CC SQ SEQUENCE 878 AA; 98070 MW; 093B13F4 CRC32;

Query Match 65.4%; Score 34; DB 1; Length 878;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DPTGHSY 9

| | | | |

Db 796 DPTNHAY 802

Search completed: December 8, 1999, 23:56:43
Job time: 17567 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 1999, 00:13:00 ; Search time 15.25 Seconds
(without alignments)
36.321 Million cell updates/sec

Title: US-08-819-669D-26
Perfect score: 52
Sequence: 1 EADDTGHSY 9

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database : SPTREMBL_10;*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	37	71.2	1032	11	Q61989		Q61989 mus musculu
2	36	69.2	2457	12	Q41965		Q41965 murine herp
3	35	67.3	1187	2	Q59278		Q59278 celluloomba
4	35	67.3	131	2	Q85701		Q85701 streptomyce
5	35	67.3	330	11	Q60763		Q60763 mus musculu
6	35	67.3	330	11	Q60761		Q60761 mus musculu
7	35	67.3	320	11	Q89006		Q89006 mus musculu
8	35	67.3	325	11	Q89010		Q89010 mus musculu
9	34	65.4	1671	1	P77933		P77933 pyrococcus
10	34	65.4	224	2	Q69955		Q69955 streptomyce
11	34	65.4	224	2	Q6995		Q6995 streptomyce
12	34	65.4	215	2	Q87935		Q87935 streptomyce
13	34	65.4	268	4	Q14969		Q14969 homo sapien
14	34	65.4	1184	4	Q75339		Q75339 homo sapien
15	34	65.4	347	4	Q75862		Q75862 homo sapien
16	34	65.4	347	4	Q00601		Q00601 homo sapien
17	34	65.4	156	5	Q23961		Q23961 drosophila
18	34	65.4	599	6	Q19112		Q19112 sus scrofa
19	34	65.4	272	11	Q35130		Q35130 rhizomys pr
20	34	65.4	267	11	Q70217		Q70217 mus musculu
21	34	65.4	3942	11	Q88737		Q88737 mus musculu
22	34	65.4	320	11	Q89009		Q89009 mus musculu
23	34	65.4	906	12	Q9YURI		Q9YURI hemorrhagic
24	34	65.4	370	13	Q91904		Q91904 xenopus lae
25	33	63.5	295	4	Q26704		Q26704 methanobact
26	33	63.5	301	1	Q59491		Q59491 pyrococcus
27	33	63.5	1086	2	Q69230		Q69230 bacillus sp
28	33	63.5	307	2	Q24828		Q24828 acneobact
29	33	63.5	288	2	Q51333		Q51333 pseudomonas

ALIGNMENTS

RESULT	1	SPTREMBL_10;	*	PRELIMINARY;	PRT;	1032 AA.
Q61989		Q61989		Q61740;		
ID		Q61989		061740;		
SC		Q61989		061740;		
DT		01-NOV-1996	(TREMBLrel.	01, Created)		
DT		01-MAY-1999	(TREMBLrel.	10, Last sequence update)		
DE		INTEGRIN ALPHA-4 SUBUNIT PRECURSOR (INTEGRIN ALPHA-IV) (VLA-4) (CD49D)				
DE		(LYMPHOCYTE-PENTER'S PATCH ADHESION MOLECULES ALPHA SUBUNIT) (LPAM)				
DE		(ALPHA SUBUNIT).				
GH		ITGA4 OR VLA-4.				
OS		Mus musculus (Mouse).				
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC		Eutheria; Rodentia; Sciurognath; Murinae; Muridae; Mus.				
RN	[1]	SEQUENCE FROM N A., AND TISSUE SPECIFICITY				
RC		STRAIN=OBA, AND NIH/SWISS; TISSUE=LEUKEMIA, AND FIBROBLAST;				
RC		RC: MEDLINE: 95290094.				
RR		DE MEIRMAN C., SCHOLLEN E., JASPERS M., ONGENA K., MATTHIJS G.,				
RA		MARYNEN P., GASSIMAN J.J.;				
RT		"Cloning and characterization of the promoter region of the murine alpha 4 integrin subunit."				
RL		DNA CELL BIOL. 13:743-754 (1994).				
RN	[2]	SEQUENCE FROM N A.				
RF		STRAIN=B6/CBA, AND NIH/SWISS; TISSUE=SPLEEN, AND FIBROBLAST;				
RC		RC: MEDLINE: 96336295.				
RX		DE MEIRMAN C., JASPERS M., SCHOLLEN E., CASSIMAN J.J.;				
RA		"The genomic structure of the murine alpha 4 integrin gene."				
RT		DNA CELL BIOL. 13:595-603 (1996).				
RL		RNA. 13(1):1-13 (1998) TO EMBL/GENBANK/DDJB DATA BANKS.				
RN	[3]	SEQUENCE FROM N A.				
RF		SEQUENCE FROM N A.				
RC		SEQUENCE FROM N A.				
RX		SEQUENCE FROM N A.				
RA		HASEGAWA M., FOOTE S.;				
RA		RA: HASEGAWA M., FOOTE S.;				
RL		RA: HASEGAWA M., FOOTE S.;				
RN	[4]	SEQUENCE OF 134-307 FROM N A.				
RF		TISSUE=MELANOMA;				
AC		ROUT U.K., ARMAND D.R.;				
RA		ROUT U.K., ARMAND D.R.;				
RL		SUBMITTED (APR-1997) TO EMBL/GENBANK/DDJB DATA BANKS.				
CC		-1- FUNCTION: THE ALPHA-4 BETA-1 INTEGRIN MEDIATES ADHESION TO ONE OR				
CC		MORE DOMAINS WITHIN THE HEPATITIS REGION OF FIBRONECTIN				
CC		INCLUDING THE ALTERNATIVELY SPLICED CS-1 REGION. VLA-4 ALSO				
CC		RECOGNIZES THE CELLULAR LIGAND ICAM-1 ON ACTIVATED ENDOTHELIAL				
CC		CELLS. IT TRIGGERS HOMOTYPIC AGGREGATION FOR MOST VLA-4-POSITIVE				
CC		LEUKOCYTE CELL LINES. VLA-4 MAY ALSO PARTICIPATE IN CYTOLYTIC				
CC		T-CELL INTERACTIONS WITH TARGET CELLS. IMPORTANT FOR CELL-CELL				
CC		ADHESION FUNCTIONS (BY SIMILARITY).				
CC		-1- FUNCTION: THE ALPHA-4 BETA-7 HETERO-DIMER INTERACTS WITH THE				
CC		LYMPHOCYTE-PENTER'S PATCH ADHESION MOLECULE MADCAM-1 AND IS				
CC		IMPORTANT FOR CELL-CELL ADHESION FUNCTIONS. VLA-4 MAY PLAY A				
CC		SUPPORTIVE ROLE IN THE HOMING OF LYMPHOCYTES TO THE PEYER'S				

CC -!- PATCHES: DIMER OF AN ALPHA AND BETA CHAIN. THE BETA CHAIN THAT ASSOCIATES WITH ALPHA-4 IS EITHER BETA-1 OR BETA-7. THE ALPHA-4 BETA-1 HETERO-DIMER IS REFERRED TO AS VLA-4 OR LPAM-2. THE ALPHA-4 BETA-7 HETERO-DIMER IS REFERRED TO AS LPAM-1 OR THE PEYER'S PATCH HOMING RECEPTOR. THE ALPHA CHAIN CAN SOMETIMES BE CLEAVED INTO TWO NON-COVALENTLY ASSOCIATED FRAGMENTS.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: THE VLA-4 INTEGRIN IS MAINLY EXPRESSED BY LYMPHOID AND MYELOID CELLS. THE ALPHA-4 BETA-7 INTEGRIN IS EXPRESSED BY PEYER'S PATCH HOMING CELLS.

CC -!- MISCELLANEOUS: THIS PROTEIN HAS 3 POTENTIAL CALCIUM-BINDING SITES.

CC -!- CALCIUM IONS MAY PLAY A ROLE IN STABILIZING THE HETERO-DIMER.

CC -!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

DR EMBL; U34800; AAB09301..1; -.

DR EMBL; U34827; AAB09330..1; JOINED.

DR EMBL; U34627; AAB09330..1; JOINED.

DR EMBL; U34429; AAB09330..1; JOINED.

DR EMBL; U34630; AAB09330..1; JOINED.

DR EMBL; U34631; AAB09330..1; JOINED.

DR EMBL; U34632; AAB09330..1; JOINED.

DR EMBL; U34633; AAB09330..1; JOINED.

DR EMBL; U34634; AAB09330..1; JOINED.

DR EMBL; U34435; AAB09330..1; JOINED.

DR EMBL; U34763; AAB09330..1; JOINED.

DR EMBL; U34764; AAB09330..1; JOINED.

DR EMBL; U34165; AAB09330..1; JOINED.

DR EMBL; U34766; AAB09330..1; JOINED.

DR EMBL; U34167; AAB09330..1; JOINED.

DR EMBL; U34168; AAB09330..1; JOINED.

DR EMBL; U34769; AAB09330..1; JOINED.

DR EMBL; U34770; AAB09330..1; JOINED.

DR EMBL; U34197; AAB09330..1; JOINED.

DR EMBL; U34198; AAB09330..1; JOINED.

DR EMBL; AF101136; AAC093388..1; -.

DR EMBL; U97151; AAC05709..1; -.

DR PFAM; MG:9603; ITGAA.

DR PROSITE; PS00357; integrin_A; 1.

KW Integrin; Cell adhesion; Glycoprotein; Transmembrane; Signal;

KW Extracellular matrix; Cytoskeleton; Calcium-binding; Polymorphism.

FT SIGNAL 1 34 1032 INTEGRIN ALPHA-4 SUBUNIT.

SQ SEQUENCE 1032 AA; 115085 MW; 27B37931 CRC32;

Query Match 2 Best Local Similarity 100.0%; Pred. No. 45; Mismatches 0; Indels 0; Gaps 0; Sequence FROM N.A.

Qy 4 PTGHSY 9 Db 29 PTGHSY 34

RESULT 2 ID 041965 PRELIMINARY; PRT; 2457 AA.

AC 041965; 01-JAN-1998 (TREMBrel. 05, Created) DT 01-JAN-1998 (TREMBrel. 05, Last sequence update) DE TEGUMENT PROTEIN. GN GAMMAHV_OF64.

OS murine herpesvirus 68. Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae. RN [1]

RP SEQUENCE FROM N.A. STRAIN=WUNS;

RX MEDLINE; 97366649.

RA VIRGIN H.M. IV, LATREILLE P., WAMSLEY P., HALLSWORTH K., WECK K.E., DAL CANTO A.J., SPECK S.H.; "Complete sequence and genomic analysis of murine gammaherpesvirus 68." J. Virol. 71:5894-5904 (1997).

RA LATREILLE P., WAMSLEY P., WATERSTON R.H.; Submitted (APR 1997) to the EMBL/GenBank/DBJ databases. EMBL; U97553; AAB6617.1; SEQUENCE 2457 AA; 273335 MW; 8DC81BBD CRC32; RP SEQUENCE FROM N.A.

RA LATREILLE P., WAMSLEY P., WATERSTON R.H.; DR U97553; AAB6617.1; SEQUENCE 2457 AA; 273335 MW; 8DC81BBD CRC32; SQ SEQUENCE FROM N.A.

Query Match 69.2% Best Local Similarity 71.4%; Pred. No. 1.8e+02; Mismatches 2; Conservative 0; Indels 0; Gaps 0; Sequence FROM N.A.

Qy 3 DPTGHSY 9 Db 1531 DPTGHTF 1537

RESULT 3 ID Q59278 PRELIMINARY; PRT; 1187 AA.

AC 059278; 01-NOV-1996 (TREMBrel. 01, Created) DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)

DT 01-MAY-1999 (TREMBrel. 10, Last annotation update) DE ENDOXYLANASE (EC 3.2.1.8) (ENDOXYLANASE) DE (1,4-BETA-D-XYLAN XYLANHYDROLASE).

GN XYNC. Cellulomonas fimi. Bacteria; Firmicutes; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas. OC [1]

RN [1] Sequence OF 1-352 FROM N.A. RX MEDLINE; 962431.

RA CLARKE J.H., DAVIDSON K., GILBERT H.J., FONTES C.M., HAZLEWOOD G.P.; RT "A modular xylanase from mesophilic Cellulomonas fimi contains the same cellulose-binding and thermostabilizing domains as xylanases from thermophilic bacteria." DR PF00331; Glyco_hydro_10; 1. KW Xylan degradation; Hydrolase; Glycosidase. SEQUENCE 1187 AA; 123378 MW; 92B3994A CRC32; RN [2] Sequence FROM N.A.

Query Match 67.3% Best Local Similarity 85.7%; Pred. No. 1.3e+02; Mismatches 0; Conservative 0; Indels 0; Gaps 0; Sequence FROM N.A.

Qy 3 DPTGHSY 9 Db 1047 DPTGTSY 1053

RESULT 4 ID 085701 PRELIMINARY; PRT; 131 AA.

AC 085701; 01-NOV-1998 (TREMBrel. 08, Created) DT 01-NOV-1998 (TREMBrel. 08, Last sequence update) DE HYPOTHETICAL (14.2 KD PROTEIN)

OS Streptomyces lividans . Actinobacteria; Actinomycetaceae; Streptomyces; Bacteria; Firmicutes; Streptomycetales; Streptomyctaceae; Streptomyces.
 OC
 RN [1] SEQUENCE FROM N.A.
 RP
 RC
 AC
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 RA DE BACKER O., VERHEYDEN A.M., MARTIN B., GODELAINE D., DE PLAEN E.,
 RA BRASSIER R., AVNER P., BOON T.;
 RT "Structure, chromosomal location, and expression pattern of three mouse genes homologous to the human MAGE genes.";
 RL Genomics 28:74-83(1995).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN TUMOURS OF VARIOUS HISTOLOGICAL TYPES BUT NOT IN NORMAL TISSUES EXCEPT TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY.
 DR EMBL; U19031; AAA86096.1; ALT-INIT.
 DR EMBL; U19032; AAA86097.1; ALT-INIT.
 DR MGD; MGI:105117; MAGE-RS2.
 DR PFAM; PF01454; MAGE; 1.
 DR Antigen; Tumor antigen.
 SQ SEQUENCE 131 AA; 14187 MW; 8321BCE1 CRC32;

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

RESULT 5
 Q60763 PRELIMINARY; PRT; 330 AA.
 ID Q60763;
 AC
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 RA DE MELANOMA ANTIGEN, RELATED SEQUENCE 2 (SMAGE-3 PROTEIN).
 GN MAGE-RS3.
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP
 SEQUENCE FROM N.A.
 STRAT= DBA/2; TISSUE=KIDNEY;
 RX MEDLINE: 96070435.
 RA DE BACKER O., VERHEYDEN A.M., MARTIN B., GODELAINE D., DE PLAEN E.,
 RA BRASSIER R., AVNER P., BOON T.;
 RT "Structure, chromosomal location, and expression pattern of three mouse genes homologous to the human MAGE genes.";
 RL Genomics 28:74-83(1995).
 DR MGD; MGI:105109; MAGE-RS3.
 DR PFAM; PF01454; MAGE; 1.
 DR PFM; PF01454; MAGE; 1.
 SQ SEQUENCE 330 AA; 35985 MW; 83AD4246 CRC32;

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

RESULT 5
 Q60763 PRELIMINARY; PRT; 330 AA.
 ID Q60763;
 AC
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAY-1999 (TREMBLrel. 08, Last sequence update)
 RA DE MELANOMA ANTIGEN RELATED SEQUENCES 1 AND 2 (SMAGE-1 PROTEIN / SMAGE-2 PROTEIN).
 GN (MAGE-RS1 OR SMAGE1) AND (MAGE-RS2 OR SMAGE2).
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

RESULT 6
 Q60761 PRELIMINARY; PRT; 330 AA.
 ID Q60761;
 AC
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAY-1999 (TREMBLrel. 08, Last sequence update)
 RA DE MELANOMA ANTIGEN RELATED SEQUENCES 1 AND 2 (SMAGE-1 PROTEIN / SMAGE-2 PROTEIN).
 GN (MAGE-RS1 OR SMAGE1) AND (MAGE-RS2 OR SMAGE2).
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

RESULT 8
 Q60761 PRELIMINARY; PRT; 330 AA.
 ID Q60761;
 AC
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAY-1999 (TREMBLrel. 08, Last sequence update)
 RA DE MELANOMA ANTIGEN RELATED SEQUENCES 1 AND 2 (SMAGE-1 PROTEIN / SMAGE-2 PROTEIN).
 GN (MAGE-RS1 OR SMAGE1) AND (MAGE-RS2 OR SMAGE2).
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

RESULT 9
 Q60761 PRELIMINARY; PRT; 330 AA.
 ID Q60761;
 AC
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAY-1999 (TREMBLrel. 08, Last sequence update)
 RA DE MELANOMA ANTIGEN RELATED SEQUENCES 1 AND 2 (SMAGE-1 PROTEIN / SMAGE-2 PROTEIN).
 GN (MAGE-RS1 OR SMAGE1) AND (MAGE-RS2 OR SMAGE2).
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

RESULT 9
 Q60761 PRELIMINARY; PRT; 330 AA.
 ID Q60761;
 AC
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAY-1999 (TREMBLrel. 08, Last sequence update)
 RA DE MELANOMA ANTIGEN RELATED SEQUENCES 1 AND 2 (SMAGE-1 PROTEIN / SMAGE-2 PROTEIN).
 GN (MAGE-RS1 OR SMAGE1) AND (MAGE-RS2 OR SMAGE2).
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

Query Match 67.3%; Score 35; DB 11; Length 330;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SQ

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=LIVER;
 RC DE PLAEN E., DE BACKER O., ARNAUD D., BONJAN B., CHOMEZ P.,
 RA MARVELANGE V., AVNER P., BALDACCI P., BABINET C., HWANG SY.,
 RA KNOWLES B., BOON T.;
 RT "A new family of mouse genes homologous to the human MAGE genes."
 DR Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AD005530; CA006584.1;
 DR PFAM: PF01454; MAGE; 1;
 DR SEQUENCE 325 AA; 36640 MW; 3B3022A3 CRC32;

Query Match 9
 Best Local Similarity 67.3%; Score 35; DB 11; Length 325;
 Matches 6; Conservative 66.7%; Pred. No. 31; Indels 1; Gaps 0;
 Qy 1 EADPTGHSY 9
 Db 155 EVDSVHSHY 163

RESULT 9
 ID P77933 PRELIMINARY; PRT; 1671 AA.
 AC P77933;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE DNA-DEPENDENT DNA POLYMERASE (EC 2.7.7.7)
 DE (DNA-DIRECTED DNA POLYMERASE) (DNA NUCLEOTIDYLTRANSFERASE
 DE (DNA-DIRECTED)) .
 GN POL.
 OS Pyrococcus sp.
 Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=RODI;
 RX MEDLINE: 98027387
 RA TARAGI M., NISHIOKA M., KAKIHARA H., KITABAYASHI M., INOUE H.,
 RA KAWAMAKI B., OKA M., IMANAKA T.;
 RT "Characterization of DNA polymerase from Pyrococcus sp. strain KOD1
 and its application to PCR".
 RL Appl. Environ. Microbiol. 63:4504-4510(1997).
 CC -; CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N
 CC DIPHOSPHATE + DNA(N).
 DR EMBL: D89671; BAA6142.1;
 DR PFAM: PF00136; DNA pol.B;
 FT CHAIN: 407 766 ENDONUCLEASE.
 KW Transferase; Nucleotidyltransferase; Endonuclease.
 FT CHAIN: 852 1388 ENDONUCLEASE.
 SEQUENCE 1671 AA; 193432 MW; 32C27AEE CRC32;

Query Match 9
 Best Local Similarity 65.4%; Score 34; DB 1; Length 1671;
 Matches 6; Conservative 66.7%; Pred. No. 2.4e+02; Indels 3; Gaps 0;
 Qy 1 EADPTGHSY 9
 Db 1616 EFPPTKHY 1624

RESULT 10
 ID O53701 PRELIMINARY; PRT; 197 AA.
 AC O53701;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE HYPOTHETICAL 21.4 KD PROTEIN.
 GN MTW036.01C;

OC Mycobacterium tuberculosis; Actinobacteria; Actinomycetales; Firmicutes; Bacteria; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC Mycobacterium tuberculosis; Actinobacteria; Actinomycetales; Firmicutes; Bacteria; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=H37RV;
 RC SEQUENCE FROM N.A.
 RA BROWN D., CHURCHER C.M.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=H37RV;
 RC SEQUENCE FROM N.A.
 RA COLE S.T.; PARKHILL J.; BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3] SEQUENCE FROM N.A.
 RP STRAIN=H37RV;
 RC SEQUENCE FROM N.A.
 RX MEDLINE: 96184548.
 RA PHILIPP W.J., POULET S., EIGLMAYER K., PASCOPELLA L., BLOOM B.R., BERGH S., BLOOM B.R., JACOBS W.R. JR., COLE S.T.;
 RA "An integrated map of the genome of the tubercle bacillus, Mycobacterium leprae." ;
 RT DR EMBL: AL021331; CAA17372.1; -.
 KW DR EMBL: AL021331; CAA17372.1; -.
 SQ SEQUENCE 197 AA; 21376 MW; FABC6607 CRC32;

Query Match 65.4%; Score 34; DB 2; Length 197;
 Best Local Similarity 71.4%; Pred. No. 28;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DPTGHSY 9
 Db 46 DPTSHAY 52

RESULT 11
 ID O65955 PRELIMINARY; PRT; 224 AA.
 AC O65955;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DE DE HYPOTHETICAL 24.1 KD PROTEIN (FRAGMENT).
 GN SC3F9.15.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Streptomyces; Streptomyces; Streptomyctaceae; Streptomyces.
 OC Actinomycetales; Streptomyctaceae; Streptomyces; Streptomyces.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=A3 (2);
 RC SEQUENCE FROM N.A.
 RA SPEGER K.J., HARRIS D.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=A3 (2);
 RC SEQUENCE FROM N.A.
 RX MEDLINE: 97000351.
 RA REDENBACH M., KIESER H.M., DENAPANTE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3 (2) chromosome." ;
 RT RL Mol. Microbiol. 21:77-96 (1996).
 RT DR EMBL: AL023662; CAA13638.1; -.
 KW Hypothetical protein.
 FT NON_TER 224 224
 SQ SEQUENCE 224 AA; 24075 MW; 75A2A272 CRC32;

Query Match 65.4%; Score 34; DB 2; Length 224;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 DPTGHSY 9
 Db 204 DPTGSSY 210

RESULT 12
 ID 087835 PRELIMINARY; PRT; 215 AA.
 AC 087835; 08. Created)
 DT 01-NOV-1998 (TREMBLrel. 08. Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08. Last annotation update)
 DE HYPOTHETICAL 24-2 KD PROTEIN (FRAGMENT).
 GN SC8A6_01.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 OC Actinomycetales; Streptomyctinae; Streptomyctaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAINA3(2);
 RA SEAGER K.J.; HARRIS D.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PARKHILL J.; BARRELL B.G.; RAJANDREAM M.A.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAINA3(2);
 RX MEDLINE: 97000351.
 RA REDENBACH M., KIESER H.M., DENAPATE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Microbiol. 21:77-96(1996).
 DR EMBL: AL031013; CAA19733.
 KW Hypothetical protein.
 FT NON-TER 1
 FT 215 AA; 215
 SQ SEQUENCE 215 AA; 24196 MW; F7643103 CRC32;

Query Match 65.4%; Score 34; DB 2; Length 215;
 Best Local Similarity 85.7%; Pred. No. 31; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 DPTGHSY 9
 Db 15 DPTGSSY 21

RESULT 13
 ID 014969 PRELIMINARY; PRT; 268 AA.
 AC 014969; 01. Created)
 DT 01-NOV-1996 (TREMBLrel. 01. Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08. Last annotation update)
 DE T(3;5)(Q25.1;P34) FUSION GENE NPM-MLF1.
 GN NPM-MLF1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96152893.

RA YONEDA-KATO N.; LOOK A.T.; KIRSTEIN M.N.; VALENTINE M.B.;
 RA RAIMONDI S.C.; COHEN K.J.; CARROLL A.J.; MORRIS S.W.;
 RR t(3;5)(Q25.1;P34) of myelodysplastic syndrome and acute myeloid
 leukemia produces a novel fusion gene, NPM-MLF1.";
 RL Oncogene 12:265-275(1996).
 DR EMBL: L49054; AAA99997.1;
 SQ SEQUENCE 268 AA; 30627 MW; F1B19980 CRC32;

Query Match 65.4%; Score 34; DB 4; Length 268;
 Best Local Similarity 71.4%; Pred. No. 39;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 DPTGHSY 9
 Db 99 DPGHNSF 105

RESULT 14
 ID 075339 PRELIMINARY;
 AC 075339; 08. Last annotation update)
 DT 01-NOV-1998 (TREMBLrel. 08. Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10. Last annotation update)
 DE CARTILAGE INTERMEDIATE LAYER PROTEIN.
 GN CILP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-ARTICULAR CARTILAGE;
 RX MEDLINE: 98389785.
 RA LORENZO P.; NEAME P.; SOMMARIN Y.; HEINEGARD D.;
 RT Cloning and deduced amino acid sequence of a novel cartilage protein
 (CILP) identifies a proform including a nucleotide
 RT pyrophosphohydrolase.";
 RL J. Biol. Chem. 273:24469-24475(1998).
 DR EMBL: AF035408; AAC33838.1; -.
 DR PFAM; PF00047 ig_1;
 DR PFAM; PF00090; tspl_1;
 DR PFAM; PF00090; tspl_1;
 SQ SEQUENCE 1184 AA; 132538 MW; 3EEFF9774 CRC32;

Query Match 65.4%; Score 34; DB 4; Length 1184;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 DPTGHSY 9
 Db 1068 DPLGHNY 1074

RESULT 15
 ID 075862 PRELIMINARY;
 AC 075862; 08. Last annotation update)
 DT 01-NOV-1998 (TREMBLrel. 08. Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10. Last annotation update)
 DE MGE-B1.
 GN MGE-B1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96152893.

RA MUZNY D.; ARENSON A.D.; ADAMS C.; BRUNDAGE E.; BUNAC C.; CARVELLI K.;
 RA CHACKO J.; CHEN J.; DI W.; DING Y.; DUGAN S.; DURBIN J.; FORCUM J.;
 RA GANESH R.; GARCIA C.; GOODMAN M.; GORRELL J.H.; HAYWOOD M.;
 RA HERNANDEZ J.; JACKSON L.; JIN S.; KAMPAL R.; KARPATHY S.; KOVAR C.;
 RA LEAL B.; LI Y.; LICHTFAROE O.; LIU W.; LOGAN O.; LU J.; LY T.;

RA MARTINEZ C.; OSWAL G.; PEREZ L.; RASHID N.D.; ROWLAND K.; SAVAGE L.
RA SCHERER S.E.; SHEN H.; SIMON M.; STOVALL K.; TIANIS K.M.; TODD J.;
RA VO Q.; WILLIAMSON A.; WORLEY K.C.; YU W.; CHINAULT C.; NELSON D.;
RA GIBBS R.A.;
RT "Direct Submission."
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC005185; AAD10634.1;
DR PFAM; PF01454; MAGE_1;
SQ SEQUENCE 347 AA; 39037 MW; 4BA34904 CRC32;

Query Match 65.4%; Score 34; DB 4; Length 347;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EADPTGHSY 9
| :.:1.:1.:1:
Db 167 EDNPSGHTY 175

Search completed: December 11, 1999, 01:16:39
Job time: 3819 sec

Result No.	Score	Query	Match Length	DB ID	Description
1	5674	US-08-819-669D-8 5674 Sequence: 1 CCGGGGACACTGGCATC.....TAATGATCTGGGTGGATTC	679419	5674	OM nucleic - nucleic search, using sw model Run on: December 10, 1999, 02:36:51 ; Search time 2290.15 Seconds (without alignments) 7879.429 Million cell updates/sec
Title: US-08-819-669D-8					
Perfect score: 5674					
Sequence: 1 CCGGGGACACTGGCATC.....TAATGATCTGGGTGGATTC					
Scoring table: IDENTITY_NUC					
Searched: 679419 seqs, 1590154680 residues					
Database :					
GenEmbl.*					
1: gb_bal;*					
2: gb_ba2;*					
3: gb_on;*					
4: gb_ov;*					
5: gb_dat;*					
6: gb_ph;*					
7: gb_p11;*					
8: gb_p12;*					
9: gb_p13;*					
10: gb_pr2;*					
11: gb_pr3;*					
12: gb_ro;*					
13: gb_st;*					
14: gb_sts;*					
15: gb_sy;*					
16: gb_un;*					
17: gb_yi;*					
18: em_fun;*					
19: em_htg;*					
20: em_hum1;*					
21: em_hum2;*					
22: em_in;*					
23: em_on;*					
24: em_or;*					
25: em_ov;*					
26: em_dat;*					
27: em_ph;*					
28: em_pl;*					
29: em_ro;*					
30: em_sts;*					
31: em_sy;*					
32: em_un;*					
33: em_v1;*					
34: gb_htg1;*					
35: gb_htg2;*					
36: gb_ini1;*					
37: gb_in2;*					
38: em_ba1;*					
39: em_ba2;*					
40: em_hum3;*					
41: em_hum4;*					
42: gb_pr4;*					
SUMMARIES					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					

Query Match Score 5674; DB 5; Length 5674;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5674; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CCGGGGACCACTGGCATCCRCGCCATACCCCCAATCCTCCCTTACGCCACCC 60
 Db 1 CCGGGGACCACTGGCATCCRCGCCATACCCCCAATCCTCCCTTACGCCACCC 60

Qy 61 ATCCAAACATCTACGCTCACCCCAAGCCAGATACTGGCTTACCCCCCTG 120
 Db 61 ATCCAAACATCTACGCTCACCCCAAGCCAGATACTGGCTTACCCCCCTG 120

Qy 121 CTCTCAACCAGGGAAAGCCAGGTGGCCAGATGTGACGCCACTTGAGCATTAGTGG 180
 Db 121 CTCTCAACCAGGGAAAGCCAGGTGGCCAGATGTGACGCCACTTGAGCATTAGTGG 180

Qy 181 TTAGAGAGAGGAGGTTTCGGTCTGGGGGGCTGAGATGGGAGGGCGG 240
 Db 181 TTAGAGAGAGGAGGTTTCGGTCTGGGGGGCTGAGATGGGAGGGCGG 240

Qy 241 CCAAGCTGTAGGGAGGAAGGTGACATGCTGGAGGACTGGAGCCACTTACCCC 300
 Db 241 CCAAGCTGTAGGGAGGAAGGTGACATGCTGGAGGACTGGAGCCACTTACCCC 300

Qy 301 AGATAGAGGACCCCAAATAATCCCTTATGCCAGTCCTGGGACCATCTGGTGGGACTTC 360
 Db 301 AGATAGAGGACCCCAAATAATCCCTTATGCCAGTCCTGGGACCATCTGGTGGGACTTC 360

Qy 361 TCAAGCTGGCCACCCCCAGCCCCCTGGCTTAACACTGGGACTCTGAAGTCAGAG 420
 Db 361 TCAAGCTGGCCACCCCCAGCCCCCTGGCTTAACACTGGGACTCTGAAGTCAGAG 420

Qy 421 CTCTGTGTGATCAGGGAAAGGGCTTAGGAGGGCTTCTGCTTAACACTGGGACTCTGAAGTCAGAC 480
 Db 421 CTCTGTGTGATCAGGGAAAGGGCTTAGGAGGGCTTCTGCTTAACACTGGGACTCTGAAGTCAGAC 480

Qy 481 CATGCTCAGGATCTCAAGGGGGCTTAAAGACCCACATCCGGTGGACCAAAC 540
 Db 481 CAGCTCAGGATCTCAAGGGGGCTTAAAGACCCACATCCGGTGGACCAAAC 540

Qy 541 CCCCACTCCAATCTCACTTCCCTGACCCAACCCCTCTATGTATTCACCCCA 600
 Db 541 CCCCACTCCAATCTCACTTCCCTGACCCAACCCCTCTATGTATTCACCCCA 600

Qy 601 CCCAACATCCCCACCCATCTCTGTGCCATCCCCACCCCTCTATGTATTCACCC 660
 Db 601 CCCAACATCCCCACCCATCTCTGTGCCATCCCCACCCCTCTATGTATTCACCC 660

Qy 661 CACCCCCACCCCCACCCACCCAGGGGACTCCACGGGAGGATCGGTTCGG 720
 Db 661 CACCCCCACCCCCACCCACCCAGGGGACTCCACGGGAGGATCGGTTCGG 720

Qy 721 CAGCGAAACATCCGGTCTGGCATGCTGCGACTGATGGCCATTCACCC 780
 Db 721 CAGCGAAACATCCGGTCTGGCATGCTGCGACTGATGGCCATTCACCC 780

Qy 781 CTCGTGAGGGCAAGGTGAGGGCTAGGGAGACTGGACCCGCCACTCCAAAATA 900
 Db 781 CTCGTGAGGGCAAGGTGAGGGCTAGGGAGACTGGACCCGCCACTCCAAAATA 900

Qy 841 GAGAGCCCAAATATTCCAGGCCGCTGAGGACCTGACGGCAACTCCAAAATA 960
 Db 841 GAGAGCCCAAATATTCCAGGCCGCTGAGGACCTGACGGCAACTCCAAAATA 960

Qy 901 CGTGTGAGGGCAAGGTGAGGGCTAGGGAGACTGGACCCGCCACTCCAAAATA 960
 Db 901 GAGAGCCCAAATATTCCAGGCCGCTGAGGACCTGACGGCAACTCCAAAATA 960

Qy 961 CGTGTGAGGGCAAGGTGAGGGCTAGGGAGACTGGACCCGCCACTCCAAAATA 1020
 Db 961 CGTGTGAGGGCAAGGTGAGGGCTAGGGAGACTGGACCCGCCACTCCAAAATA 1020

Qy 1021 TTCTCCCAAAGCTCTGGGATCAGGGTAGGTTAGGAGGG 1080

Db 1021 TTCTCCCAAAGCTCTGGGATCAGGGTAGGTTAGGAGGG 1080

Qy 1081 GCAGGGCACAGGCTCTGGGATCAGGGTAGGTTAGGAGGG 1140
 Db 1081 GCAGGGCACAGGCTCTGGGATCAGGGTAGGTTAGGAGGG 1140

Qy 1141 CCAGACTGACATCCAAATCCCAACTCCACCCATTCGATTCCTGCACCAAC 1200

Db 1141 CCAGACTGACATCCAAATCCCAACTCCACCCATTCGATTCCTGCACCAAC 1200

Qy 1201 CCATCTCTCTGACTCTACCTCCACTCCACCCATTCGATTCCTGCACCAAC 1260

Db 1201 CCATCTCTCTGACTCTACCTCCACTCCACCCATTCGATTCCTGCACCAAC 1260

Qy 1261 ACCCTCCAGCCCCAGGCCACCCAACTCCCTCTGGCACCTACCTGCCCTAAC 1320
 Db 1261 ACCCTCCAGCCCCAGGCCACCCAACTCCCTCTGGCACCTACCTGCCCTAAC 1320

Qy 1321 CCCACCTCTCATCTCTCATGTCCTCCACTCCATGCCCTCCCCATTCGCGAAATCTC 1380

Db 1321 CCCACCTCTCATCTCTCATGTCCTCCACTCCATGCCCTCCCCATTCGCGAAATCTC 1380

Qy 1381 GTTTGGGGAGTGGCTCTGGCTCTGGGGGATGTGAACCACTGACT 1440
 Db 1381 GTTTGGGGAGTGGCTCTGGCTCTGGGGGATGTGAACCACTGACT 1440

Qy 1441 TGAACTCACAGATCTGGAGAGGGCCAGGTGATTAATGGTCTGAGGGGGCTGTGAG 1500
 Db 1441 TGAACTCACAGATCTGGAGAGGGCCAGGTGATTAATGGTCTGAGGGGGCTGTGAG 1500

Qy 1501 ATCCACTGAGGGAGTGGCTCTGGCTCTGGGGGAAAGTGTGAGGGAGG 1560
 Db 1501 ATCCACTGAGGGAGTGGCTCTGGCTCTGGGGGAAAGTGTGAGGGAGG 1560

Qy 1561 ACTGAGGGGCCACACCCCACTGAGTGGCCCAAATATGTCAGTACCCCTGCTG 1620
 Db 1561 ACTGAGGGGCCACACCCCACTGAGTGGCCCAAATATGTCAGTACCCCTGCTG 1620

Qy 1621 CGAGCCCTGAGCCACCCGGAGACATGTCAGTCTGGCTCTGGGGGGCTG 1680
 Db 1621 CGAGCCCTGAGCCACCCGGAGACATGTCAGTCTGGCTCTGGGGGGCTG 1680

Qy 1681 CACTGCCACTTAACCCAGGGCAATCTGAGTGGCCCAAATATGTCAGTACCCCTGCTG 1740
 Db 1681 CACTGCCACTTAACCCAGGGCAATCTGAGTGGCCCAAATATGTCAGTACCCCTGCTG 1740

Qy 1741 GGTCAGGGAGGGAGGGCTGAGGTCAGCATCCCGGCCATTAAGGGTCAAG 1800
 Db 1741 GGTCAGGGAGGGAGGGCTGAGGTCAGCATCCCGGCCATTAAGGGTCAAG 1800

Qy 1801 ACCCTGGAGGGAACTGAGGGTCTCCCTCATCTGGTCAAGAACCTCTGGCTG 1860
 Db 1801 ACCCTGGAGGGAACTGAGGGTCTCCCTCATCTGGTCAAGAACCTCTGGCTG 1860

Qy 1861 CCACTCACATCCCATACCTTACCCCTAACCCCAACCTCTGGTCAAGAACCTCTGGCTG 1920

Db 1861 CCACTCACATCCCATACCTTACCCCTAACCCCAACCTCTGGTCAAGAACCTCTGGCTG 1920

Qy 1921 TAACCCAGGGAGGGCAAGGGATGGGGCACTGGGACTCTGGTCAAGAACCTCTGGCTG 1980
 Db 1921 TAACCCAGGGAGGGCAAGGGATGGGGCACTGGGACTCTGGTCAAGAACCTCTGGCTG 1980

Qy 1981 GGTCGTGATGGGGAGGGCTGAGGGGGCTCAGGGGGAGGGGGCCCTAC 2040
 Db 1981 GGTCGTGATGGGGAGGGCTGAGGGGGCTCAGGGGGAGGGGGCCCTAC 2040

Qy 2041 TGGAGATGGGGAGGGCTGAGGGGGCTCAGGGGGAGGGGGCCCTAC 2100
 Db 2041 TGGAGATGGGGAGGGCTGAGGGGGCTCAGGGGGAGGGGGCCCTAC 2100

Qy 2101 ACTGAGGGTGCACACTTGTGCTCTGGGATCAGGGACTGATGGGG 2160

Qy	4321	CTCTGAGTCCTTGCAGCTGGCTTTGGCATTTGACCGAACCCGAGCCCCGCCA	4.380
Db	4321	CTCTGAGTCCTTGCAGCTGGCTTTGGCATTTGACCGAACCCGAGCCCCGCCA	4.380
Qy	4381	CTCTTAATGCTCTTGTCACTTGCCCTAGGTCTCTCTTATGATGGCTGTATAATCA	4.440
Db	4381	CTCTTAATGCTCTTGTCACTTGCCCTAGGTCTCTCTTATGATGGCTGTATAATCA	4.440
Qy	4441	GATCATGCCAAAGAACAGGCTTCCGTATAATTGTCCTGGTCATGATGGCATTTGAGGGGG	4.500
Db	4441	GATCATGCCAAAGAACAGGCTTCCGTATAATTGTCCTGGTCATGATGGCATTTGAGGGGG	4.500
Qy	4501	CCATGCTCTGTAGGGAGAAATCTGGAGGAGCTGAGTGTGATGGGGTGTATGATGGAG	4.560
Db	4501	CCATGCTCTGTAGGGAGAAATCTGGAGGAGCTGAGTGTGATGGGGTGTATGATGGAG	4.560
Qy	4561	GGAGCACAGTGCCCTATGGGAGGCCAGGAAGCTGCTACCCAAAGATTGTCAGGGAAA	4.620
Db	4561	GGAGCACAGTGCCCTATGGGAGGCCAGGAAGCTGCTACCCAAAGATTGTCAGGGAAA	4.620
Qy	4621	GTACCTGAGTAGGGCAGTGCGGACAGTGATGCCAGCGCTATGAGTCCTGTGGGT	4.680
Db	4621	GTACCTGAGTAGGGCAGTGCGGACAGTGATGCCAGCGCTATGAGTCCTGTGGGT	4.680
Qy	4681	CCAAGGGCCCTCCTGAAACCAGGTATGTCAGGCTTGTGAAAGTCCTGAGATGTCAGT	4.740
Db	4681	CCAAGGGCCCTCCTGAAACCAGGTATGTCAGGCTTGTGAAAGTCCTGAGATGTCAGT	4.740
Qy	4741	GCAAGACTTCGCTTTCTCCCATCCTCTGGTGAAGGCAGCTTGTAGAGGGAGAGAG	4.800
Db	4741	GCAAGACTTCGCTTTCTCCCATCCTCTGGTGAAGGCAGCTTGTAGAGGGAGAGAG	4.800
Qy	4801	GGAGTCGAGCATGAGTGGAGCCAGGGCAGTGGAGGGACTGGCCAGTGGCACCTT	4.860
Db	4801	GGAGTCGAGCATGAGTGGAGCCAGGGCAGTGGAGGGACTGGCCAGTGGCACCTT	4.860
Qy	4861	CCAGGGGGGTCCAGAGCTTCCCCTGCCTGCTGTGACATGAGGCCATCTCTACTCT	4.920
Db	4861	CCAGGGGGGTCCAGAGCTTCCCCTGCCTGCTGTGACATGAGGCCATCTCTACTCT	4.920
Qy	4921	GAAGAGACGGTCAGTGTCTCACTAGTGTAGTTCTGTCATGTTGCTGAGGATT	4.980
Db	4921	GAAGAGACGGTCAGTGTCTCACTAGTGTAGTTCTGTCATGTTGCTGAGGATT	4.980
Qy	4981	TATCTTGTGTTCTTTGGAAATTGTTGAATGAGCAGGCACTAACAGTCTGTTGATGAAAC	5.040
Db	4981	TATCTTGTGTTCTTTGGAAATTGTTGAATGAGCAGGCACTAACAGTCTGTTGATGAAAC	5.040
Qy	5041	TTCAGCATCCAAGTTGAATGAGCAGGCACTAACAGTCTGTTGATGAAATTTGTTGAGGAAAT	5.160
Db	5041	TTCAGCATCCAAGTTGAATGAGCAGGCACTAACAGTCTGTTGATGAAATTTGTTGAGGAAAT	5.160
Qy	5101	TAAGAGTCTGTGTTTATTCACTGGAAATCTTATCTTGTGATGGGAAAT	5.220
Db	5101	TAAGAGTCTGTGTTTATTCACTGGAAATCTTATCTTGTGATGGGAAAT	5.220
Qy	5221	AGAACTTAAGAAATTAAAGATGAGTCATTCTGGCTTACCTCTGTTGATGGGAAAT	5.280
Db	5221	AGAACTTAAGAAATTAAAGATGAGTCATTCTGGCTTACCTCTGTTGATGGGAAAT	5.280
Qy	5281	ATTTTAAAGATATGACACCTGGATTCTTGTGTTGAGAATGTAAGGAAAT	5.340
Db	5281	ATTTTAAAGATATGACACCTGGATTCTTGTGTTGAGAATGTAAGGAAAT	5.340
Qy	5341	TAATCTGAAATAAGAAATTCTCTGTTCACTGGCTTCTTCTCCATGCACTGAGCA	5.400
Db	5341	TAATCTGAAATAAGAAATTCTCTGTTCACTGGCTTCTTCTCCATGCACTGAGCA	5.400
Qy	5401	TCTGCTTTGGAAAGCCCTGGGGTAGCTGAGCATGCTTAAGGCAAGACTOATAC	5.460

Eb	5401	TCTGGCTTGTGGAGGCCCTGGTTAGTAGGAGATGCTAAGGTAAAGCTTAACGTCAGTCACTGAGGGCTCCGGTGAAGATGTC	5460
Qy	5461	CCACCCATTAGGGCTGTAAGGCTCAGGAGCTCCAGTAATCGAGGTGGCAAAAGATGTC	5522
Db	5461	CCACCCATTAGGGCTGAGCTAGCTAGAGCTGAACTGGAGCTGGAGATGTC	5522
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGGAGGGTGAAGGGCTCCGGTGAAGATGTC	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGGAGGGTGAAGGGCTCCGGTGAAGATGTC	5580
Qy	5581	GTTGAGGTCAATGGCTTGAGCTGGGCATTTGGCTTGGAAACTGGAGTTCCTCT	5640
Db	5581	GTTGAGGTCAATGGCTTGAGCTGGGCATTTGGCTTGGAAACTGGAGTTCCTCT	5640
Qy	5641	GGGGAGCTGATTGTAAATGATCTGGGTGGATCC	5674
Db	5641	GGGGAGCTGATTGTAAATGATCTGGGTGGATCC	5674
RESULT	2		
LOCUS	I36923	136923	5674 bp
DEFINITION		Sequence 8 from patent US 5612201.	DNA
ACCESSION	I36923		
NTD	92084883		
VERSION	I36923.1	GI:2084883	
KEYWORDS			
SOURCE	Unknown:		
ORGANISM	Unknown:		
	Unclassified.		
REFERENCE	1 (bases 1 to 5674)		
AUTHORS	De Paeen,B., Boon-Palleur,T., Lethe,B., Szikora,J., De Smet,C.		
Chomcz,P.			
TITLE	Isolated nucleic acid molecules useful in determining expression		
a tumor rejection antigen precursor			
JOURNAL	US 5612201-A 8 18-MAR-1997;		
FEATURES	Location/Qualifiers		
source	1..5674	/organism="unknown"	
BASE COUNT	1276	a: 1644 c: 1569 g: 1185 t:	
ORIGIN			
Query Match	100.0%	Score 5674; DB 5; Length 5674;	
Best Local Similarity	100.0%	Pred. No. 0; Mismatches 0; Indels 0; Gaps	
Matches 5674; Conservative	0;		
Qy	1	CCGGGGCACCACTGGATCCCTCCCCCTACCCCCCAATCCCCCTTACGGCACCC	60
Db	1	CCGGGGCACCACTGGATCCCTCCCCCTACCCCCCAATCCCCCTTACGGCACCC	60
Qy	61	ATCCAAACATCTTCAGCTCACCCAGGCCAGGAGCAATCCGGTTCACCCCTG	120
Db	61	ATCCAAACATCTTCAGCTCACCCAGGCCAGGAGCAATCCGGTTCACCCCTG	120
Qy	121	CTCTCAACCCAGGGAGCCAGGTGCCAGATGTGACGCCACTGACTTGACCATAGTGG	180
Db	121	CTCTCAACCCAGGGAGCCAGGTGCCAGATGTGACGCCACTGACTTGACCATAGTGG	180
Qy	181	TTAGAGAAACGGAGTTCGGCTGAGGGGGCTGAGATCGTGGAGGGAGCGGG	240
Db	181	TTAGAGAAACGGAGTTCGGCTGAGGGGGCTGAGATCGTGGAGGGAGCGGG	240
Qy	241	CCCAGCTCTGAAAGGAGCAAGGTGACATGCTGAGGGAGACTGGAGCCACTAACCC	300
Db	241	CCCAGCTCTGAAAGGAGCAAGGTGACATGCTGAGGGAGACTGGAGCCACTAACCC	300
Qy	301	AGATAGGAGCCCAAATAATCCTTCATGCCAGTCCTGGACCACATCTGGGGTGGACTTC	360
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Qy	361	TCAGGCTGGCCACCCAGGCCCTTGTGCTTAAACACTGGGAGCTGAAGTCAGAG	420

Db	361	TCAAGGCTGGCCACCCCCAGCCCCCTCTGTAAACACTGGTAAACACTGGGACTCGAAGTCAGAG	420	Db	1441	TGAACCTCACAGATCTGGAGAAGCCAGGTCAATTAAATGGTTCTGAGGGGGCTTGAG	1500
Qy	421	CCTCGTGTGATCAGGGAGGGCTGCTTAGGAGGGCAGCTGCCAGACAT	480	Qy	1501	TATCCACTAGTGAGGTGGTTTAAGGCTGTGAGGTGAGTGTGCTAGGGGG	1560
Db	421	CCTCGTGTGATCAGGGAGGGCTGCTAGGAGGGCAGCTGCCAGACAT	480	Db	1501	TATCCACTAGGGCATCTGGAGTGTGCTAGGCTGTGAGGTGAGTGTGCTAGGGGG	1560
Qy	481	CATGCTCAGGATCTCAGGGGGCTGAGGGTCCCTAGACCCCACCTGGTACCCAAC	540	Qy	1561	ACTGAGGGCACACCCAGTAGATGCCCAAATGATCAGTACCCCTGTG	1620
Db	481	CATGCTCAGGATCTCAGGGGGCTGAGGGTCCCTAGACCCCACCTGGTACCCAAC	540	Db	1561	ACTGAGGGCACACCCAGTAGATGCCCAAATGATCAGTACCCCTGTG	1620
Qy	541	CCCCACTCCAAATGCTCACTCCGTACCTCAACCCCC	600	Qy	1621	CCAGGCCCCGGACACCCGGCAGACATGTGAGTGGGACACCCCCCGTCCGTC	1680
Db	541	CCCCACTCCAAATGCTCACTCCGTACCTCAACCCCC	600	Db	1621	CCAGGCCCCGGACACCCGGCAGACATGTGAGTGGGACACCCCCCGTCCGTC	1680
Qy	601	CCCCACATCCCCACCCCCATCCCTAACCCCTGATGCCCATTCACCT	660	Qy	1681	CACTGCCACTTAACCCAGGGCAATCTGAGTCACCTTAATGTAACGGGCAGGGT	1740
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Qy	661	CACCCCCACCCCCACCCCCACCCCAACCCCAACCCAGGATCCGGTTCCG	720	Qy	1741	GCTCAGGGAGGGAGGGCAGGCACTGGTCAAGTCAGTACCTATGTACGGGGAGGT	1800
Db	661	CACCCCCACCCCCACCCCCACCCCAACCCAGGATTCGGTTCCG	720	Db	1741	GCTCAGGGAGGGAGGGCACTGGTCAAGTCAGTACCTATGTACGGGGAGGT	1800
Qy	721	CCAGAAACATCCGGGTGCGGATGTGCGCACTGAATGGCGCATGAGA	780	Qy	1801	ACCTGGAGGGAGACTGGGGTICCCCAACCCACACCTCTCTCATTCACGCCACC	1860
Db	721	CCAGAAACATCCGGGTGCGGATGTGCGCACTGAATGGCGCATGAGA	780	Db	1801	ACCTGGAGGGAGACTGGGGTICCCCAACCCACACCTCTCTCATTCACGCCACC	1860
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Db	781	GAAGCGAGGTTCATCTGAGGGACGGCTAGATTGGCGAAGGACCCAGG	840	Db	1861	CCACTCACATCCCCATACCTACCCCTAACCTAACCTAACCTAACCT	1920
Qy	841	CTCTGTGAGGGCAAGGTGAGGGCTAGGGAGGACTGAGGCCCGCCACTCCAATA	900	Qy	1921	TCAACCCACGGAAAGCCACGGGAATGGGGCCAGGCACCTGGATCTGATCCCACATCA	1980
Db	841	CTCTGTGAGGGCAAGGTGAGGGCTAGGGAGGACTGAGGCCCGCCACTCCAATA	900	Db	1921	TCAACCCACGGAAAGCCACGGGAATGGGGCCAGGCACCTGGATCTGATCCCACATCA	1980
Qy	901	GAGGCCCAAAATAATTGCGCCCTTGCGCCAGGCTTGCCCAACCCGGGAAAGA	960	Qy	1981	GGGTCTGATGGGGAGGGCTGAGGGGCTCAGGGGAGGGAGGGCCCTAC	2040
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Qy	961	CGTCCTCAGGCTGGCTGCCAGACCCCTGTCTGAGGACACCGAGTC	1020	Qy	2041	TGCGAGATGGGGAGGGCTCAGGGACCCCTGAGGACCCCTGAGGACCTGCTGAG	2100
Db	961	CGTCCTCAGGCTGGCTGCCAGACCCCTGTCTGAGGACACCGAGTC	1020	Db	2041	TGCGAGATGGGGAGGGCTCAGGGACCCCTGAGGACCCCTGAGGACCTGCTGAG	2100
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Db	1021	TCTCTCCCCAAGGCTGCTGGAAATCAGGGTGGCTGAGGACGGAGG	1080	Db	2101	ACTGAGGGTGCACACTCTGGCTCAAGAACTGAGGACTCATGGATGGGG	2160
Qy	1081	GCAGGGCACAGGTCTGCCAGCATGAGTCAACCTTGTGCTGAGGAGG	1140	Qy	2161	CTGGGACCCAGGGCTGCAAGGAGGAGGAGGAGGACTCAGGGGACCTT	2220
Db	1081	GCAGGGCACAGGTCTGCCAGCATGAGTCAACCTTGTGCTGAGGAGG	1140	Db	2161	CTGGGACCCAGGGCTGCAAGGAGGAGGACTCAGGGGACCTT	2220
Qy	1141	CCAGAAGCTGCACTCCAACTCCACCTGGCATCCACCTGGGACCC	1200	Qy	2221	GGATTCGGATCATGGTGGCTGATCTGGGAGGACTCAGGGGACCTGCTGAG	2280
Db	1141	CCAGAAGCTGCACTCCAACTCCACCTGGCATCCACCTGGGACCC	1200	Db	2221	GGATTCGGATCATGGTGGCTGATCTGGGAGGACTCAGGGGACCTGCTGAG	2280
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Db	1441	TGAACCTCACAGATCTGAGGAGCCAGTTCAATTAAATGGTCTGAGGGGGCTGAG	1500	Db	2521	CAGCAGGAAACTGGGGCCCTCAGGGAGATGGGTAAAGGGGGATGTCT	2580

		ORGANISM	Homo sapiens
Db	4741	GCAAGACTTCGCTTCTTCATCCATCCTCGCTGACAGCTTGAGAGGGAGAG	4800
Qy	4801	GGAGCTGAGCATGAGTGTGACCAAAGCCAACTGGAGGGGACTGGCCAGTGACCTT	4860
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Qy	4861	CCAGGGCGCTCCAGGCTTCCTGCCTGACATGGGCCATTCTTCACTT	4920
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Qy	4921	GAAGAGGGTCAAGCTTCTCAGTAGTTCTGAAATTGTTAAGGGATGGTGAAC	4980
Db	4921	GAAGAGGGTCAAGCTTCTCAGTAGTTCTGAAATTGTTAAGGGATGGTGAAC	4980
Qy	4981	TATCTTGTCTTGTGAATTGTCAAATTGTTAAGGGATGGTGAATGAA	5040
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Qy	5041	TTCAGCATCCAAAGTTTATGAACTGACACAGCTCACAGTCTGTATACTTAA	5100
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Qy	5101	TAGAGCTTGTCTTATTAGATGGAAATCTGAAATTGAGGAAATGAGGATAA	5160
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Db	5521	CTCTAAAGATGAGGAAAGTGAAGAGGGTGAAGGGCTGGCTGGTGAAGATG	5580
Qy	5581	GTGGAGCTCAATGGCCCTGAGCTGGGCAATTGGGAAGTGCAGTTCCCTCT	5640
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LOCUS		Human chromosome X clone Qc15B1	DNA sequence.
DEFINITION			
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NID	92078526		
VERSION	U82672.1		
KEYWORDS	HIG.		
SOURCE	human		

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library Match Score 5532.0
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matches 5640; Conservative 0; Mismatch 0

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Dy	6551	ACCACAGGGAGGAAGTGGGGGCCCTCAGGGAGATGGGCTTTGGGTAAAGGGGGAT	6495
Db	2577	GTC TACTCATGTCAGGGAGATGGGGCTTGAGGAAGAACAGGGCTGCAGGATAAGAT	2636
Dy	6494	GTC TACTCATGTCAGGGAGATGGGGCTTGAGGAAGAACAGGGCTGCAGGATAAGAT	6435
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Dy	6374	ACCTCACCCCAGGATGGGCTT-TTTCATCCTGGGGCAGGGTGG	6316
Db	2757	ACCTATTCAGGGTGTGACTCAGGGTCAAGTGGGACCCATCTGGTAAGACAG	2816
Dy	6315	ACCTATTCAGGGTGTGACTCAGGGTCAAGTGGGACCCATCTGGTAAGACAG	6256
Dy	2817	AGGGGTCAGGATCGGCAATCGGCAATCGGCAATCGGCAATCGGCAATCGGCA	2876
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Dy	2937	AGAGACATGGCTGGCCGCTGGGAGGCTTGCAAGAACATTAGCCCTGGGTAGGT	2996
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Dy	3177	GTTTGTCCCCCTGTCGCTTCAATCCCTATCATGGATGAGTCAGCTTGATGATT	3236
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Dy	3417	TCTCTTCCTGGAGGATGCCAGGAGGACTGAGACAGTATCTTC	3476
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Db	4395	GGGTCCAAGGGCCTCCCTGAAACCACATCTAATGAAAGTCAGTCAAGG	4336	NID VERSION KEYWORD SOURCE ORGANISM	94567140 AF134576.1 HTG. Homo sapiens
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Db	4335	TCACTGCGAAAGCTTCGCTTTCTTCCCCTGCCTGAAAGCAGCTTGAGAGGG	4276	Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Qy	4796	AAGAGGGAGTCAGCATGAGTTCGAGCAAGGCCAGTGGAGGGACTGGCCAGTGC	4855	1 (bases 1 to 49375)	
Db	4275	AAGAGGGAGTCAGCATGAGTTCGAGCAAGGCCAGTGGCCAGTGGCCAGTGC	4216	Gloeckner G. and Rosenthal A.	
Qy	4856	ACCTTCCAGGGCGGTCAAGCATGAGTTCGAGCAAGGCCAGTGGCCAGTGGCCAGTGC	4915	Sequence of three cosmids of human Xq28 (16c3, 3g5, 3h5) containing MAGE genes	
Db	4215	ACCTTCCAGGGCGGTCAAGCATGAGTTCGAGCAAGGCCAGTGGCCAGTGC	4156	Unpublished	
Qy	4916	ACCTGAAAGAGGAGGGTCAAGTGTCTCAGTAGTAGGTCTATTGGGTGACTTGG	4975	2 (bases 1 to 49375)	
Db	4155	ACCTGAAAGAGGAGGGTCAAGTGTCTCAGTAGTAGGTCTATTGGGTGACTTGG	4096	Authors REFERENCE	
Qy	4976	AGTTTATCTTCTTCTTCTTGAATGTTCAATGTTTAAAGGTGTTGAA	5035	Direct Submission	
Db	4095	AGATTATCTTCTTCTTGAATGTTCAATGTTTAAAGGTGTTGAA	4036	JOURNAL	
Qy	5036	TGACTTCAGCAAGTCAGCTTGAGCAAGCTCTGTATATACTT	5095	Submitted (12-MR-1999) Genome Analysis, Institute for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany	
Db	4035	TGACTTCAGCAAGTCAGCTTGAGCAAGCTCTGTATATACTT	3976	FEATURES	
Qy	5096	AGGGTAAGACTCTGCTTTATTCAAGTGGAAATCCATCTTATTGGTAATGGG	5155	Source	
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LOCUS				/rpt_unit="cccac"	
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				/note="GC score = 44.00 (895bp)"	

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Db	27536	GTCAGGGCTGTGAGGGAAAGGACTAAGGGACTCAGGGACCTCCAGGCCACC	27595	-----	28554
Qy	299	CCAGATAGGGACCCAAATAATCC-----CTTCACTGCAGTCCTGGAGCATCTGG	349	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27596	CCAGATAGGGCCCAAATAATCCAGCACTACTCTGGCAAGCCCTAACACCTGG	27655	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	350	TGTTGACTCTCAAGCTGGCCACCCCGACCCCT-----TGCTGCTTAACCCA	400	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27656	GGGGGACTCTCACTCTGGCAACCTGGCAACCCCTGGCTTAAGGCC	27715	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	401	CTGGGACTC-GAACTCAAGCTCCGGTGTGATCAGGAAGGGCTTACAGGGCAG	459	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27716	CAAGGGACTCTGAGCTCAGGCTCTGGTAACAGGAGGGCTTAGAGGGCAG	27775	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	460	CGTCCAGGGCTGCCCAGACATCATGCTCAGGATTCTCAAGGGGGCTGAGGGTCCCTAAG	519	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27776	TGGCAAGCTGCGAGGATCACTAGGAACTCTAACATGGCAAGCTGAGGGCTGAGGGCCAAAC	27835	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	520	ACCC--CACTCCGGTACCCCACTCTCACTGGCTACTCCGTGACCAACCCCC	576	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27836	CCCCATTCCTCCATCCCCATCCCCATCCCCATCCCCATCCCCATCCCCA	27895	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	577	TCTCTGTTGTCATCAACCCCCAACCCCCAACCCCCAACCTCTAACCCCTGATGC	636	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27896	CCAGAACCCCTATCCCCAACAGAACCCCTATCTGGCCACTCCCCAACACGTCATCCC	27955	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	637	CCATCGGCCCA-GCCATTCACCCCTCACCCCCAACCCCCAACGCCACTCCACCC	695	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	27956	TACTCCTCACCATCCCCATCCCCATCCCCATCCCCATCCCCATCCCC	28015	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	696	CCACCCAGGAGATCCG-----	742	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28016	ACACCTGGAGAAATCGGTTCTGCTCTGCTTCAACCCAGGAAATCCGGTGGACCA	28075	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	743	GATGPGAGCCACTACTCTGGCAATGTTGCGGAGAGGAGGTTCTGTGAG	802	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28076	GATGNGGTGGCACATGTTGTCACATTTGAGTCGGAGAGAACGGCTCTCTGAG	28135	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	803	GGACGGCTGAGATGGCTGGCCGAAGGAACCTGAGCCAGGGCTCTGAGGGAGG	862	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28136	GGCGAGC-TGAGATCAGCTGGAGGGAGCTGGCTCTGGCTCTGGAGGTGAG	28194	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	863	AGGCTGAGGGAGGTGAGGACCCGCACTCAATAAGAACCCCCAAATAATCCAG	- 921	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28195	ATGCTGAGGGAGACTAAGGAGGATTCACCCCTGGTAGTGAGCCAAATAATCCAGT	28254	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	921	-CCAGCCCCCTGCTGCCACGGCTGGCCACCCGGAAAGAACGTCAGCTGGCTG	979	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28255	CCACCTCTCTGGCTGACCATCTGGACCTCAAGGGCAGACTCTTGGTGGGCCACC	28314	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	980	CCAGACCCCCCTGCTCCAAAAGCCTGAGAGACACCAGGTTCTCCCCAAGGCTCTGGAA	1039	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28315	CCAGCTCCCCACCCCTTAAGCCGAGGGAA-	28553	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	1040	TCAGGGTGTGACCGGGCAGACTGGTAGAGAGGGACGGCTCTGGCC	1099	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28354	ACAGACCTGCTGATGACCGGGCAGACTGTAGAGAGGGCTGTCAGCTGGCTCTGCC	28413	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	1100	AGCATCAAGATCACCCAGGGAGGGCTGTCAGCTGGCCCAAGACTGCACTCCAATC	1159	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28414	AGAAACAACTGCAAGGAACTTAAGGAAAGCTGAGGCTTACCC-	28457	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	1160	CCACTCCCCATCCCCATCCCTACTCTGCACTCCCCAACCCCCATCTCTGAGCTAC	1219	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28457	--	28459	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	1220	CTCCACCCCCATCCCCATCCCTACTCTGCACTCCCCAACCCCCATCTCTGAGCTAC	1279	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Db	28460	CCCAAACCTCATCTGCTCTACCTCTGGCCACCCCTACACCCCCATCTC	1339	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA
Qy	1280	AGCCCCAACCTCTGGCACCTCACCCCACTGCCCCAACCCCCATCTCTGAGCTAC	1339	-----	1340 TGTCGCCCACTCCCCATGCCATCGCTGGAGAACCTGGTT-TGCCCCTGCTCA

2377	GCCCCAAGATGTCGCCCTTCATGAGGACTGGGATATCCCGCTCAGAAAGGGGC	2436
29585	GCCCCAATGTGTCGCCATTATCATGAAAGTGGGATA- CCTGGCTCAGAAAGGGAC	29643
2437	TCCACAGTCGCTGGCTGTCCTTTACTAGCCTCTAGGGGACAGATGGGG	2496
29644	CCACAGTCGCTGGCTGTCCTCTAGGGGACAGATGGGG	29703
2497	TATGTTCACTTCTACGTGTTACACAGCAGGAAGTGGGGCCCTAGGGAGATGGG	2556
29704	TATGTTCACTTCTACGTGTTACACAGCAGGAAGTGGGGCCCTAGGGAGATGGG	23763
2557	TCTTGGGTAAGGGGGATGTCATCTACGTGTTACGGGATGGGGTGGAGCACAG	2616
29764	TCTTGGCAGTAAGGGGGCTATGTGTCATCTACGGGGTTAGGTGAGGATGGCAG	29823
2617	GCGCTGGCAACCTCATTTGTGCCAACAGGAAAGAGTTAACAGCCCAGAGA	2676
29824	GCCCCATCAAG- -ATGAGATAAACCACTACCCAGAGA	29879
2677	CCAAAGGGTCAGCCCTGGACACTCA	2727
29880	CCAAAGGGTCACTCCGACACCCATGTGGGGTACAGGGATGTASC-TCCATCTCAT	29338
2728	TCTGTGTTCAGATCTGGCTGGGAGGACTCATCTAGGGGTGACTCAGTCAC	2877
29939	TCTGTGTTCAGATCTGGGGGTGAACTTGTCTCCGGGATACTCAGTCAC	29998
2788	GTAGGGACCCCATCTGGGATGAGCTGAGGAGTGGGATTCGGGT	2847
29999	AGAGGGGCCATCTGGGATGAGCTGAGGAGTGGGATTCGGGT	30058
2848	GAGGAACATGAGGGAGGACTGGGTTACCCAGGACAGAACACTGAGGGAGACTGCACA	2907
30059	GAGGAACATGAGGGAGCATTGGGGCACCCCTGGCCAGAACAGATGGGCTCAG	30118
2908	GAATAGCCCTGCCCTGCTGTCACCCAGAGCATGGGCTGGGCTCCGGGT	2957
30119	GAATATCNGCCCTGCTGCTGTCACCCAGAGCATGGGCTGGTCTGTCAGT	30178
2968	CCTCCCT-GTGGGATATTGAGTCAGGAGCCTGGGGCTGGTCTGAGGG	3025
30179	CCCCCCCACCTACCTGGGATATTGGTGTCAAGGATGGGGTCTTGTIC	30237
3026	CTGCGCTCAGGTCAGTAGGGAGGCTCCAGGCTGGGCTGGGCTGGGAGG	3085
3038	CTGCACTCAGGTCAGTAGGGAGGCTCCAGGCTGGGCTGGGAGG	30297
3086	ACGGGGACCTCACCCAGGACATTAATTCCAAATGAAATTGATTCCTGCTGCC	3145
30298	ACCGAGTCCTCACCCAGGACATTAATGCAATTCAATGCTTCCTGTCCT	30357
3146	TCCCA-AGGACCTAGGTCAGGAGGCTGGGAGGCTGGGAGG	3204
30358	TCCCAAGGAGGCTGGGAGGCTGGGAGGCTGGGAGG	30414
3205	TATCATGATGTAACCTGTTGGATTTCTCAGACCAGAAAAGGGCAGGATCCAGG	3264
30415	TATCAGGATGTAACCTGTTGGATTTCTCAGACCAGAAAAGGGCAGGATCCAGG	30474
3265	CCCTGGGAGGAAAAATAAGGGCCCTGGCTGAGAACAGGGGGTATCCTCAGTCATGTA	3324
30475	CTCTGGCAGGACCTCACAGATTCAAGCTGGGAGGCTGGGAGGCTGGGAGG	30534
3325	GAGTGGGAGGTCACAGTCAGGCTGGGAGGCTGGGAGGCTGGGAGG	3384
30535	GGTGTGGAGACCTCACAGATTCAAGCTGGGAGGCTGGGAGGCTGGGAGG	30594
3385	GCTTGGGAGGTCACCCCTGAGGGCCCTGGATTCCTGGAGCTCCAGAAACAGG	3444
30595	TGCTGGT-TAATGAGATCATGCCAACAGGGGCTCTGATAATGCTCTGATG	30654
3445	CAGTGGGCTTGGTGGAGCAGTATCTCAGGAGGAGATGGAGCACAG- ---	35014
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Qy	3727 C-AAGGAAGAGATCTGTAAGTAGGGCTTCTGTTAGAGTCTCAGGTCCTCTGCT	3785
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Qy	3846 CCACACTCCCTGGCTGCTGGCTGAGGAGTCATGTCAGTGTCTGAGGAGTCAGTGC	3905
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Qy	3906 ACTGCAAGGCCCTGGGCCCCAACAGAGGCCCTGCTGCTGCTGCTGCTG	3965
Db	31135 ACTGEAGGAGGAGTGCCTGGCTGCTGGCTGAGGAGTCATGTCAGTGTCTGAGGAGTCAGTGC	31194
Qy	3966 AGGCCTGCACC- - - - - TCCCTCTCTCTGCTGCTGCTGCTGCTG	4004
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Qy	4005 CCCTGGGGAGGTGCCTGGCTGCTGGCTGCTGGCTGCTGCTGCTGCTG	4064
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Qy	4065 CGCCCTTCCACCTACCATCAACTCTGAGGCTGGGTTCCAGGACCT	4124
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Qy	4125 GCGCTGGAGAGGGGGCCAAAGCACCTCTGTTGGAGCTCTGTTGGAGCTAA	4184
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Qy	4185 TCACTAAGGAGTGGCTGATTTGGTGTCTGGCTCTCAATATGAGCAGGGAGC	4244
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Qy	4245 CAGTCACAAGGAGGAGAATGTTGGAGTGTGTCATCAAATACTGAGCAGTCCTGTTCTG	4304
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Qy	4305 AGATCTTCGCAAAAGCCCTCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTG	4364
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Db	31673 TGCTGGT-TAATGAGATCATGCCAACAGGGGCTCTGATAATGCTCTGATG	31730
Ov	4485 TTGCAATGGAGGGGGCCCATGCTCTGGAGGAGAAATCTGGAGGAGCTGCTGAGCTGATGG	4544

	Base COUNT	polyA_signal	polyA_site	Query Match	Score	DB	9;	Length	11495;
Best Local Similarity	46	8%		Pred No; 0;					
Matches 4231; conservative	73	6%		Mismatches 1100; Indels 416;					
Matches	4231;			Gaps	50;				
y	21	CCTCCCCCACCACCCCCATCCCTTACCCCACCATCCAAAGATCTTCACGGTC	b	80					
y	5969	CCAGCACCCCTATCCTCCCAAACCCCCACTACCCCTATGTCCTCATCCCCAAC	b	6028					
y	81	ACCCCGAGGCCAAGGCCAGAACTCCGGTTACCCCTGCCTCAACCCAGGAAGC	b	139					
y	6029	ACCACTATCCCATCCAGTTGAATGCCATTCCGGTTCAACCCAGGAAGGT	b	6088					
y	140	CAGGTGCCAGATGTGACCCACTGACTCTGAGCTTAACTGGTTAGAGAA	b	199					
y	6089	CAGGTCCGGATGTGATCCAGTGTGCAATTGGGGTTAGAGAACGTAGCTG	b	6148					
y	200	TGGTCTGAGGGGGGGCTTGAGATGGTGGTGGAAAGGGGCCA-GCTCTGT	b	258					
y	6149	TCACTCTGCAGGGAGCTGGATGGTGGAAAGGGGAGGGAAAGGGT	b	6208					
y	259	CAAGTGACATGGCTGAGGGAGCT--GAGGACCCACTTACCCAGATA	b	315					
y	6209	CATGTGAGAGTGTGGAGAAAGTGGGAGCTCAGCCAGATA	b	6268					
y	3116	AATATCTCCACTCTGGACCACTCTGGACCATCTGGTGGTGGACTCT	b	366					
y	6269	AATATCCTGGACCCCCCTCTGGCTCAGCTGGCCACCCGGGAGCTCTG	b	6328					
y	367	TGGCCACCCCCAGCCCCCTGGCTTAACCACTGGGACTCTGA	b	426					
y	6329	TGGGACGGCCACCCCCCTGGCTGAAGCCGGAGCTATGGGACTCAG	b	6388					
y	4227	GTGATCAGGGAGGGCTGCTTAGAGAGGGCAGGGTCCAGGGCT	b	486					
y	6389	GTGATCAGGGACTGTGGGGT-----AGGCTGTGAGGCA	b	6436					
y	487	CAGGATTCTCAAGGGGGCTGAGGGTCCCTAAGCCCCACTCCGTGAC	b	546					
y	6437	CAGGACCCATGGAGAGGGCTGAGGTCCCCA--CCCCCATCCTTAC	b	6493					
y	547	TCCATGCTACCTCCGTGACCTCCCTCTCATGTGTCATGCCAAC	b	606					
y	6494	TCCCCATCTGCACTCC-----TACCCCCATCCCTACCCCC	b	6527					
y	607	ATCCCCACCCATCCCCATCCCCATCCCCATCCCCATCCCCATCCCC	b	666					
y	6528	ATCCCCACCTCTCATCCCCATCTGCCCCATCCCCAACCCCCATCCCC	b	6587					
y	667	CACCCCCACCCCCACGCCCACCTCCACCCCCACCCAGGAGATCG	b	725					
y	6588	CACCCCCATCTCATCCCCATCTGCCCCATCCCCAACCCCCATCCCC	b	6647					
y	726	AAACATCCGGGGCTGGGGATGTGAGGCCACATGACTGTG	b	785					
y	6648	CAAGCCCTGGGGCCGGGTGATGCCACTGACTGTGAAATGAGGT	b	6707					
y	786	GAGGTTCATTCTGAGGGACGGCTGAGGGAGACTGAGGACCCCC	b	845					
y	6708	GAGGTTCGGTCTGGATGGTGGG-TTGGATCGCAAGGGAGGTG	b	6766					
y	846	TGAGGAGGGAAAGTGAAGGCTGAGGGAGACTGAGGACCCCC	b	905					
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 De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B., Lurquin,C.,
 Brasseur,R., Chomez,P., De Backer,O., Aveneville,W. and Boon,T.
 TITLE Structure, chromosomal organization, and expression of 12 genes of
 the MAGE family
 JOURNAL Immunogenetics 40 (5), 360-369 (1994)
 MEDLINE 95012457
 REFERENCE 2 (bases 1 to 4736)
 AUTHORS De Plaen,E.
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FEATURES	source	Query Match	Score	DB 9:	Length
base count		42.7%	2422.8;	4741;	
reference	De Plaen, E.	Best Local Similarity	75.7%;	Pred. No. 0;	
authors	Direct Submission	Matches	3726;	Mismatches	882;
title	Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for			Indels	314;
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Db	2355	GTGAGTCCTCCATGGCTTCACTAATGTCAGGCTGGGATCTGAGG	2411
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						Eutheria; Primates; Catarrhini; Hominidae; Homo.
						(bases 785 to 1286)
						van der Brugge, P., Traversari, C., Chomez, P., Lurquin, C., De
						Plen, E., Van den Eynde, B., Knuth, A. and Boon, T.
						TITLE
						a gene encoding an antigen recognized by cytolytic T lymphocytes on
						a human melanoma
						Science 254, 1643-1647 (1991)
						JOURNAL
						MEDLINE
						910866861
						REFERENCE 2
						(bases 1 to 2420)
						AUTHORS
						van der Brugge, P.
						JOURNAL
						Submitted (05-FEB-1992) Pierre van der Brugge, Ludwig Institute
						for Cancer Research, Brussels Branch, Avenue Hippocrate, 74, UCL
						7439, Brussels, B-1200, Belgium
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AUTHORS	Schattetroy, R., Rosenthal, A., Drescher, B. and Schattetroy, R.
JOURNAL	Submitted (07-MAY-1997) Genome Analysis, Institut für Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
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Db 49563 AACCAAAGGGTCAAGCTGACCTCACCTGAGGTGGTAACAGGATGTGGC 49621

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Db 51772 TGGCCAGTGCACCTTCAGGGCCATCCATTAGCTTCACTGCCCTGTGTTATATGAG 51831
Qy 4905 GCCCCATTCTT-CACTCTGAAGAGCGCGTCAGTAGTAGTTCTCAGTAGTAGTTCTGCTTA 4962
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Qy 5615 GGCTTTGGGAAATGTCAGTTCTGGGGAGCTGGTATGATCTGGGGATCC 5674
Db 52528 GGATCTGGAACCTCGAGTCTGCTGATGCTGAGGCTGATCTGAGGCTGATCTGATGCCCCGGGGTCC 52587

REFERENCE 2 (bases 1 to 37781)
AUTHORS Gloeckner,G., Rosenthal,A., Drescher,B., Weber,J. and Schattrevoy,R.
TITLE Direct Submission
JOURNAL Submitted (17-oct-1997) Genome Analysis, Institut for Molecular
FEATURES Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
source Location/Qualifiers
source 1_37781
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RESULT 14
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DEFINITION Homo sapiens chromosome X clone 58F6 map Xq28, complete sequence.
ACCESSION AF030261
NID 97571136
VERSION 1
KEYWORD HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37781)
AUTHORS Gloeckner,G., Nordsiek,G., Drescher,B., Schattrevoy,R., Knob,A. and
Rosenthal,A.
TITLE Sequence of cosmid 58F6 from Xq28 containing two MAGE genes
JOURNAL Unpublished

Db	12572	CGGCCACCCCGCCGGTCTAACCGCAGGGAACTCTGGTAAGAGCTTTGTGACCAG	12513
Dy	1732	GCGAGGTTGTCAGGAGGGACTGGCCAGGCATAGGICAGATCCCAGGGATT	1791
Db	12512	GCGAGGCTGTGTTAGAAGT	-----
Dy	1792	AGGTCTAGGACCTGGGAGGGAACTGCTCTCATCTCC	1851
Db	12465	AAGTCAGGCCAAAGGGACTGAGGAACCCATACCTAACATCC	12406
Dy	1852	-----	-----
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Dy	1877	ACCTACCCCCAACCCACATCTGTAGAAAT-----	-----
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JOURNAL Unpublished (1997)
2 (bases 1 to 48574)
AUTHORS Drescher, B., Rosenthal, A., Drescher, B. and Schattbovy, R.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
Biotechnology, Beuttenbergrstrasse 11, Jena 07745, Germany
FEATURES Location/Qualifiers
source 1..48574
organism "Homo sapiens"
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Db	16585	GGAGGGTGTGGTAAAGATGTAGTCAGGAGGGGGATCTACTCATGAGGAACAC	16631
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Qy	3673	CA-GGGACAGGCCAACCCAGGACAGGATTCCTGGAGGCCACAGGGACCAAG	3731
Db	18607	GAGGGGACGGTGGACAGTGGGAGGACTGGGAGG-----ATTGAGG	18658
Qy	3732	AGAGATCTGTAAGTAGGCCTTGTAGTCAAG-----GTTCACTGTCAGCTGA	3786
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 Db 19978 ACAAATGGTGGATGAACCTCAGCATCCAAGTATTGAAACAGTACACATAGTG 20037
 Qy 5081 CTGTTATAGTATAAGGTTAAGGTTAAGTGTGTATTACAGATTGGAAATCCATTCT 5110
 Db 20038 CTGTTATAGTATAAGGTTAAGGTTAAGAAGTGTGTATTACAGATTGGAAATCCATTCT 20097
 Qy 5141 ATTGTTGAAATT-GGATAATAACAGCAGTGAAATAAGTACTTAAAGT---GAAA 5194
 Db 20098 ATTGTTGAGTTGTCACATATAACAGCAGTGAAATAATGTTATGTTATGTCCTATATGTGAACG 20157
 Qy 5195 ATGGCAGTAAATAGATGAGGATAAGAACATAAGAAATAAGATAGTCAATTCTTG 5254
 Db 20158 AATTAGCAGTAAATACATGATAAGGAAC-----TCAAAAGATACTTAAATCTTG 20209
 Qy 5255 CCTTATACCCAGCTTATCTGTTAAAGATAATATGCAATCCGATTCCCT 5314
 Db 20210 CCTTATACCCAGCTTATATGTTAAAGATAATATGCAATCCGATTCCCT 20257
 Qy 5315 GGCTTCTTGTAGAATGTAAGGAAATAAATCTGATAAAGAATTCTCCCTGTTCACTGG 5374
 Db 20258 TGCTTCTTGTAGAATGCAAAAGAAATAATCTGATAAATACTCTTCTGTTCACTGG 20317
 Qy 5375 CTCTTCTCCATGCACTGAGCATCTGCTTTTGGAGGCCCTGGGTAGTAGTGGAA 5434
 Db 20318 CTCAATTCTTACCCATTCACTCAGCATCTGCTCTGGAGGCCCTGGG--TAGTAGTGGG 20375
 Qy 5435 GATGTTAGTAAGGCAAGTCAATCCACCCATAGGTCGAGTGTAGGTGAGTGCAG 5494
 Db 20376 GATTCATAAGGTAAGGCAAGTCAACGCTTACCCATAGGTCATAGGTCTAGGAGGTGCAG 20435
 Qy 5495 TCACGTAATCCAGGTGCAACATGTCCTCTAAAGATGTTAGGAAAGTGTAGGAGGGGTG 5554
 Db 20436 TCATGTAATTAAAGGTTGGCGAAGTGTCTAGGAGTGTAGGAAATGTANGACAGGGTG 20495
 Qy 5555 AGGGTGTGGGCTCCGGGTAGAGTGGAGTGGCAATGCCCTGAGCAGGGCATTTC 5614
 Db 20496 AGGGTGTGGGCTCCAGGTGAGGTGCTGCTGCTGCTGCTGCAATTGGCAATTTC 20554
 Qy 5615 GCCTTGGAAACATGAGTCTCTGGCGAGCTGATGTTGATGTTGATCTGGTGTGATCC 5674
 Db 20555 GGATCAGGGAAACTGAGTCTCTGGCGAGCTGATGTTGATGTTGATCTGGTGTGATCC 20614

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Qy	421	CTCCGTGATCAGGGAAAGGGCTGCCTAGGAGGGCAGCTCAGGCTCAGGTCAGACAT	480	Qy	1501	ATCCACTGAGGAGTGGTTAGGCTCTGTGAGGGCAAGTGATGCTGAGGGAGG	1560
Db	421	CTCGTGTGATCAGGGAAAGGGCTGCCTAGGAGGGCAGCTCAGGTCAGACAT	480	Db	1501	ATCCACTGAGGAGTGGTTAGGCTCTGTGAGGGCAAGTGATGCTGAGGGAGG	1560
Qy	481	CATGCTCAGGATCTCAGGGAGGCTGAGGGCTCCTAGGGAAAGGGCTGCCTAGGTCAGACAT	540	Qy	1561	ACTGAGGAGGACACCCAGGTAGATGCCCAAAATGATCCAGTACACCCCTGCT	1620
Db	481	CATGCTCAGGATCTCAGGGAGGCTGAGGGCTCCTAGGGAAAGGGCTGCCTAGGTCAGACAT	540	Db	1561	ACTGAGGAGGACACCCAGGTAGATGCCCAAAATGATCCAGTACACCCCTGCT	1620
Qy	541	CCCACTCCATCTCCTACTCCCCGTGACCCAACCCCCTTCATTTGCTATTCCACCCCCA	600	Qy	1621	CCAGCCCTGACCCGGCCAGGACAGATGCTCACCTGGACCACCCCGCTCCGCTC	1680
Db	541	CCCACTCCATCTCCTACTCCCCGTGACCCAACCCCCTTCATTTGCTATTCCACCCCCA	600	Db	1621	CCAGCCCTGACCCGGCCAGGACAGATGCTCACCTGGACCACCCCGCTCCGCTC	1680
Qy	601	CCCAACATCCCCAACCCCATCTCAACCCCTGATGCCCATCCCCAGCCATTCCACCC	660	Qy	1681	CACTGCCACTTAACCCACGGCAATCTGTAGTCATGCTTATGTGACCGGGCAGGT	1740
Db	601	CCCAACATCCCCAACCCCATCTCAACCCCTGATGCCCATCCCCAGCCATTCCACCC	660	Db	1681	CACTGCCACTTAACCCACGGCAATCTGTAGTCATGCTTATGTGACCGGGCAGGT	1740
Qy	661	CACCCCCAACCCCCACCGCCACTCCACCCACCCAGGATCGGTCCCG	720	Qy	1741	GGTCAGGAGGGCAGGGCAGGCATCAAGGTCAGGATCCCCCGCATTAGGTGAGG	1800
Db	661	CACCCCCAACCCCCACCCACCCACCCACCCAGGATCGGTCCCG	720	Db	1741	GGTCAGGAGGGCAGGGCAGGCATCAAGGTCAGGATCCCCCGCATTAGGTGAGG	1800
Qy	721	CCAGGAAACATCGGGTCCGGATGTGCGCACTGACTTGCCATGTCAGGAGAGA	780	Qy	1801	ACCCCTGGAGGAACACTAGGGTTCCCAACCCACACTGTCCTCATCTCCAC	1860
Db	721	CCAGGAAACATCGGGTCCGGATGTGCGCACTGACTTGCCATGTCAGGAGAGA	780	Db	1801	ACCCCTGGAGGAACACTAGGGTTCCCAACCCACACTGTCCTCATCTCCAC	1860
Qy	781	GAAGCAGGTTTACATTGTGAGGAGCCGGTAGAGTGGCGCTAAGGTGGCAGG	840	Qy	1861	CCACTCACATCCCATACCTACCCCTAACCCCAACCTCATCTGTCAGAATCCCCTGCT	1920
Db	781	GAAGCAGGTTTACATTGTGAGGAGCCGGTAGAGTGGCGCTAAGGTGGCAGG	840	Db	1861	CCACTCACATCCCATACCTAACCCCTAACCCCAACCTCATCTGTCAGAATCCCCTGCT	1920
Qy	841	CTCTGTGAGGGCAAGGTGAGGGACTGAGGCCACTCCAAATA	900	Qy	1921	TGACCCGGAAAGCCAGGGATGGCCAGGACTGGGACTCTGACGTCCTCCATCA	1980
Db	841	CTCTGTGAGGGCAAGGTGAGGGACTGAGGCCACTCCAAATA	900	Db	1921	TGACCCGGAAAGCCAGGGATGGCCAGGACTGGGACTCTGACGTCCTCCATCA	1980
Qy	901	GAGAGCCCCAAATAATTCCAGCCCCCTTGTGCCAGCCCCGGGAGA	960	Qy	1981	GGCTCTGATGGGGGAGGGGCTTGTGACGGCCCTCTGGGAGGAGGGCCCTAC	2040
Db	901	GAGAGCCCCAAATAATTCCAGCCCCCTTGTGCCAGCCCCGGGAGA	960	Db	1981	GGCTCTGATGGGGGAGGGCTTGTGACGGCCCTCTGGGAGGAGGGCCCTAC	2040
Qy	961	CGCTCTAGCTGGCTGCCCTGCCCCAGCCCCCTGTCTCAAAGGCTTGAGACACAGCTC	1020	Qy	2041	TGGGAGATGAGGGGGCTCAGGGACCCCTAGGACACCCCTAGGACACCCGAC	2100
Db	961	CGCTCTAGCTGGCTGCCCTGCCCCAGCCCCCTGTCTCAAAGGCTTGAGACACAGCTC	1020	Db	2041	TGGGAGATGAGGGGGCTCAGGGACCCCTAGGACACCCGACCCCTGTCTGAG	2100
Qy	1021	TCTCTCCCAAGCTGGATCAGGGTAGGACTGTGTCAGGAGG	1080	Qy	2101	ACTGAGGCTGCACACTCTGGCTCAAGAACCTGGGACTCTGAGTGTGATGGG	2160
Db	1021	TCTCTCCCAAGCTGGATCAGGGTAGGACTGTGTCAGGAGG	1080	Db	2101	ACTGAGGCTGCACACTCTGGCTCAAGAACCTGGGACTCTGAGTGTGATGGG	2160
Qy	1081	GCAGGGCACAGGTCTGGCAGGGATCAAGATGACCCCCACTCCACCCCAAC	1140	Qy	2161	GTGGGACCCAGCTGAGGGCTTACCGGAGGAAGGGAGGGACTCAGGGACCT	2220
Db	1081	GCAGGGCACAGGTCTGGCAGGGATCAAGATGACCCCCACTCCACCCCAAC	1140	Db	2161	GTGGGACCCAGCTGAGGGCTTACCGGAGGAAGGGAGGGACTCAGGGACCT	2220
Qy	1141	CCAGAGCTGACTCCAATCCCCACTCCACCCCATGACCCCCAC	1200	Qy	2221	GGATCCAGATCAGTGTGACCTGGGACCTGGCCACATATG	2280
Db	1141	CCAGAGCTGACTCCAATCCCCACTCCACCCCATGACCCCCAC	1200	Db	2221	GGATCCAGATCAGTGTGACCTGGGACCTGGCCACATATG	2280
Qy	1201	CCGATCTCTCAGCTACCCCTACCCCTACTCCCTACCTGACCA	1260	Qy	2281	GCCCATATTCTGCACTCTGGTACAGGACAGCTGAGTGTGAGAAGTGGGC	2340
Db	1201	CCGATCTCTCAGCTACCCCTACCCCTACTCCCTACCTGACCA	1260	Db	2281	GCCCATATTCTGCACTCTGGTACAGGACAGCTGAGTGTGAGAAGTGGGC	2340
Qy	1261	ACCCCTGGCCAGGGCACCCAAACCCCTGCCCCACTGCCCCAAC	1320	Qy	2341	TCAGGTCAACAGGGAGGAGTCCAGGATCCATATGCCCAAGATCTGCCCTCATG	2400
Db	1261	ACCCCTGGCCAGGGCACCCAAACCCCTGCCCCACTGCCCCAAC	1320	Db	2341	TCAGGTCAACAGGGAGGAGTCCAGGATCCATATGCCCAAGATCTGCCCTCATG	2400
Qy	1321	CCACCCCTCATCTCTCATGCCCCACTCCATGCCCTCCCCAAC	1380	Qy	2401	AGGACTGGGATATCCCGGCTCAGAAAAGGGACCTCCACACAGCTGGCTGCCCC	2460
Db	1321	CCACCCCTCATCTCTCATGCCCCACTCCATGCCCTCCCCAAC	1380	Db	2401	AGGACTGGGATATCCCGGCTCAGAAAAGGGACCTCCACACAGCTGGCTGCCCC	2460
Qy	1381	GGTTGGCCCTGCTCAACCCAGGAGGCCCTGAGGAGGCGCTGAG	1440	Qy	2461	TTAGTACTCTGGGACAGATGGGTATGGCTCATCTGATGGTACCA	2520
Db	1381	GGTTGGCCCTGCTCAACCCAGGAGGCCCTGAGGAGGCGCTGAG	1440	Db	2461	TTAGTACTCTGGGACAGATGGGTATGGCTCATCTGATGGTACCA	2520
Qy	1441	TGAACTCTACAGATCTGAGAGGCCAGTTCAATTATGGCTCTGAGGGCGCTGAG	1500	Qy	2521	CAGGAGGAAGTGGGGCCCTCAGGGAGAAGGGGATGTC	2580
Db	1441	TGAACTCTACAGATCTGAGAGGCCAGTTCAATTATGGCTCTGAGGGCGCTGAG	1500	Db	2521	CAGGAGGAAGTGGGGCCCTCAGGGAGAAGGGGATGTC	2580
Qy	1441	TGAACTCTACAGATCTGAGAGGCCAGTTCAATTATGGCTCTGAGGGCGCTGAG	1500	Qy	2581	ACTCATGTCAGGGAAATTGGGGTTGAGGAAGCACGGGCTGGCAGGAATAAAGATGAGT	2640

		Db	2581	ACTCATGTCAGGAAATTGGGGTTGAGAAGGACAGCGCTGGCAAGAAATAAGATGAGT	2640		Db	3661	CCTTCAGGTTTCAGGGACAGGCCAACCCAGAGGACAGGATTCCTGGAGCCACAGAG	3720
Oy	2641	GAGACAGACAAGGCTATTGGAAATTCCACACCCCCAGAACCCAGGGTCAAGGGCACACC	2700	Oy	3721	GAGACAGACAAGGAAATTGGGTAGCTGGCTTCAGGAAATAAGATGAGT	3780			
Db	2641	GAGACAGACAAGGCTATTGGAAATTCCACACCCCCAGAACCCAGGGTCAAGGGCACACC	2700	Db	3721	GAGACAGACAAGGAAATTGGGTAGCTGGCTTCAGGAAATAAGATGAGT	3780			
Oy	2701	TGACCCAGGATGGGCTCTTTCATCCTGTTCCAGATGGGAGGTGAGGACCT	2760	Oy	3781	ACCTGAGGCCCTCACACACTCCCTCTCCAGGGCTTGTTGCTCATGTCAGGCT	3840			
Db	2701	TGACCCAGGATGGGCTCTTTCATCCTGTTCCAGATGGGAGGTGAGGACCT	2760	Db	3781	ACCTGAGGCCCTCACACACTCCCTCTCCAGGGCTTGTTGCTCATGTCAGGCT	3840			
Oy	2761	CATTCTCAGGGTGAATCAGTGAAGGACCCCCTATCTGGTCAAAGACAGAGCG	2820	Oy	3841	CCTGCCAACACTCTGGCTGTGCCCTGAGAGAGTCATCATGTCAGGAGGAG	3900			
Db	2761	CATTCTCAGGGTGAATCAGTGAAGGACCCCCTATCTGGTCAAAGACAGAGCG	2820	Db	3841	CCTGCCAACACTCTGGCTGTGCCCTGAGAGAGTCATCATGTCAGGAGGAG	3900			
Oy	2821	GTCCCAGGATCTGCCATGCGTTGGGTGAGGAACATGAGGGAGGACTGAGGTTACCCAG	2880	Oy	3901	TCTGCACTTCAGGCCCTGGAGGCCAACAAAGGGCCCTGGCTGGGTG	3960			
Db	2821	GTCCCAGGATCTGCCATGCGTTGGGTGAGGAACATGAGGGAGGACTGAGGTTACCCAG	2880	Db	3901	TCTGCACTTCAGGCCCTGGAGGCCAACAAAGGGCCCTGGCTGGGTG	3960			
Oy	2881	GACCAAGAACACTGAGGAGAACATGCCAGAACATAGCCCTGGTCACCCCAGAG	2940	Oy	3961	TCTGCACTTCAGGCCCTGGAGGCCAACAAAGGGCCCTGGCTGGGTG	4020			
Db	2881	GACCAAGAACACTGAGGAGAACATGCCAGAACATAGCCCTGGTCACCCCAGAG	2940	Db	3961	TCTGCACTTCAGGCCCTGGAGGCCAACAAAGGGCCCTGGCTGGGTG	4020			
Oy	2941	ACGATGGGCTGGCCGRTGCCAGGTTCTCGGTTATCTGGATCATGTCAGGG	3000	Oy	4021	CACTGCTGGGTAACAGATCTCGGTTCTGGATCATGTCAGGGCTCCCTTCCACTAC	4080			
Db	2941	ACGATGGGCTGGCCGRTGCCAGGTTCTCGGAGGCTCTCGGTATCTGGATCATGTCAGGG	3000	Db	4021	CACTGCTGGGTAACAGATCTCGGTTCTGGATCATGTCAGGGCTCCCTTCCACTAC	4080			
Oy	3001	ACGGGGAGGGCCTGGCTCTGAGAAGGGCTCGCCTAGTGAAGGGAGCCTCCAGGCC	3060	Oy	4081	CATCAACTCTACTCGACAGGAAACCAAGGGCTGGCTGGAGGAGGG	4140			
Db	3001	ACGGGGAGGGCCTGGCTCTGAGAAGGGAGCAGGAGGAGGAGGAGGAGGCC	3060	Db	4081	CATCAACTCTACTCGACAGGAAACCAAGGGCTGGCTGGAGGAGGG	4140			
Oy	3061	CIGCCAGAGTAAGGTGAGGACCCTACCCAGGGACCATTAATTCCAT	3120	Oy	4141	GCCAAGGCACCCCTGATCTGGCTGGAGCTTCCTCCAGGAGCTGGTGC	4200			
Db	3061	CIGCCAGAGTAAGGTGAGGACCCTACCCAGGGACACATTAATTCCAT	3120	Db	4141	GCCAAGGCACCCCTGATCTGGCTGGAGCTTCCTCCAGGAGCTGGTGC	4200			
Oy	3121	GAATTGATACTCTGCTGCCCTCCAGGACCTAGGCCAGTGTGGCATGTT	3180	Oy	4201	TGATTGGTTGGTTCTCTGCTCAAAATATGAGCCAGGAGGCCAGTACAAGGAGA	4260			
Db	3121	GAATTGATACTCTGCTGCCCTCCAGGACCTAGGCCAGTGTGGCATGTT	3180	Db	4201	TGATTGGTTGGTTCTGCTCAAAATATGAGCCAGGAGGCCAGTACAAGGAGA	4260			
Oy	3181	GTCCCCCTCTGCTCTTCCATTCTGATGGATTTCTCAG	3240	Oy	4261	AATGCTGGAGAAGTGTCACTAAATACTCAAGGACTGTTCTCTGAGATCTGGCAAGGC	4320			
Db	3181	GTCCCCCTCTGCTCTTCCATTCTGATGGATTTCTCAG	3240	Db	4261	AATGCTGGAGAAGTGTCACTAAATACTCAAGGACTGTTCTCTGAGATCTGGCAAGGC	4320			
Oy	3241	ACAGCAAAGGGCAGGATCCAGGGCCCTGGCAGGAAANTATAAGGGCCCTGGCTGAGAA	3300	Oy	4321	CCTGACTCCTGAGCTGGCTGAGCTGGCTGGAGGAGCACACCCACCGSCCA	4380			
Db	3241	ACAGCAAAGGGCAGGATCCAGGGCCCTGGCAGGAAANTATAAGGGCCCTGGCTGAGAA	3300	Db	4321	CCTGACTCCTGAGCTGGCTGAGCTGGCTGGAGGAGCACACCCACCGSCCA	4380			
Oy	3301	CAGAGGGGTATCCACTGCTGAGTGGGATGTCAAGGTCCAGCCCACCCCTCTG	3360	Oy	4381	CCTCTATGCTCTGCTGAGCTGGCTAGCTCTCTGCTGAGCTGGTGTGATANTCA	4440			
Db	3301	CAGAGGGGTATCCACTGCTGAGTGGGATGTCAAGGTCCAGGCTGGATCTCCTCTG	3360	Db	4381	CCTCTATGCTCTGCTGAGCTGGCTAGCTCTCTGCTGAGCTGGTGTGATANTCA	4440			
Oy	3361	CTAGGACTGAGAACCCAGGCTGGCTGCTGGCTCACAGAGTATCTCAGTC	3420	Oy	4441	GATCATGCCAGACAGCTTCCTGATAATTCTCTGCTGATTCATGGCC	4500			
Db	3361	CTAGGACTGAGAACCCAGGCTGGCTGCTGGCTCACAGAGTATCTCAGTC	3420	Db	4441	GATCATGCCAGACAGCTTCCTGATAATTCTCTGCTGATTCATGGCC	4500			
Oy	3421	CTTCCTGAGCTCCAGGACCTGAGCTGGCTGCTGGCTGAGCTGGCT	3480	Oy	4501	CCATGCTCTGAGGAGGAATCTGGAGGAGCTGACTGCTGGAGGTTGTATGTC	4560			
Db	3421	CTTCCTGAGCTCCAGGACCTGAGCTGGCTGCTGGCTGAGCTGGCT	3480	Db	4501	CCATGCTCTGAGGAGGAATCTGGAGGAGCTGACTGCTGGAGGTTGTATGTC	4560			
Oy	3481	ACAGAGGAGATGCAAGGGTGTGGCAAGTGAATGTTGCCCTGAAATCACCAA	3540	Oy	4561	GGAGCAGACTGCTGAGCTGGCTGAGCTGGCTCACCCAGAGTGGTCAGGAA	4620			
Db	3481	ACAGAGGAGATGCAAGGGTGTGGCAAGTGAATGTTGCCCTGAAATCACCAA	3540	Db	4561	GGAGCAGACTGCTGAGCTGGCTGAGCTGGCTCACCCAGAGTGGTCAGGAA	4620			
Oy	3541	GGCCCCACCTGCCACAGGACACATAGGACTCACAGAGTCTGGCTCACCTCCACTG	3600	Oy	4621	GTACCTGGAGTAGGGAGGTGGCTGAGCTGGCTGAGCTGGCTGAGT	4680			
Db	3541	GGCCCCACCTGCCACAGGACACATAGGACTCACAGAGTCTGGCTCACCTCCACTG	3600	Db	4621	GTACCTGGAGTAGGGAGGTGGCTGAGCTGGCTGAGCTGGCTGAGT	4680			
Oy	3601	TCACTGCTGAGTAACTGACCTCTGCTGCCCTGAGTACCCCTCACCTCT	3660	Oy	4681	CCAAGGGCCCTGCTGAAACCAAGGCTCTGAGCTGGCTGAAACAGCTTGTAGT	4740			
Db	3601	TCACTGCTGAGTAACTGACCTCTGCTGCCCTGAGTACCCCTCACCTCT	3660	Db	4681	CCAAGGGCCCTGCTGAAACCAAGGCTCTGAGCTGGCTGAAACAGCTTGTAGT	4740			
Oy	3661	CCCTCAGGTTCAAGGGACAGGCCAACCCAGGAGCAGGATTCCTGGAGCCAGAG	3720	Oy	4741	GGAGAGTGTGCTGCTGCTGAGGAGGAGAGCAGCTTGTAGT	4800			
Db	3661	CCCTCAGGTTCAAGGGACAGGCCAACCCAGGAGCAGGATTCCTGGAGCCAGAG	3720	Db	4741	GGAGAGTGTGCTGCTGAGGAGGAGAGCAGCTTGTAGT	4800			

Qy	4801	GGAGTCTGAGCATGAGTGGCAAGGCCAAGGGCAGTGGGAGGGACTGGCCAGTGCACCTT	4860		/tag= a
Db	4801	GGAGTCTGAGCATGAGTGGCAAGGCCAAGGGCAGTGGGAGGGACTGGCCAGTGCACCTT	4860	FT	W09220356-A.
Db	4861	CCAGGGCGGTCCAGCAGTCCTGGCTCTGGCTGACATGGCCATTCTTCACCT	4920	PN	26-NOV-1992;
Qy	4861	CCAGGGCGGTCCAGCAGTCCTGGCTCTGGCTGACATGGCCATTCTTCACCT	4920	PD	22-MAY-1992; i04354.
Db	4861	CCAGGGCGGTCCAGCAGTCCTGGCTCTGGCTGACATGGCCATTCTTCACCT	4920	PF	23-MAY-1991; US-705702.
Db	4861	CCAGGGCGGTCCAGCAGTCCTGGCTCTGGCTGACATGGCCATTCTTCACCT	4920	PR	09-JUL-1991; US-728838.
Qy	4921	GAAGAGAGCGGTCACTGGTCTCTAGTAGTGGTCACTGGGACTGGGAGATT	4980	PR	23-SEP-1991; US-764364.
Db	4921	GAAGAGAGCGGTCACTGGTCTCTAGTAGTGGTCACTGGGACTGGGAGATT	4980	PR	12-DEC-1991; US-807043.
Qy	4981	TATCTTTGTTCTCTTTGGATTTGGTCAATGGTCAATGGTCAATGGTCAATGG	5040	PA	(LUW-) LUDWIG INST CANCER RES.
Db	4981	TATCTTTGTTCTCTTTGGATTTGGTCAATGGTCAATGGTCAATGGTCAATGG	5040	PI	Boon T., Chomez P., De Pler E., Lurquin C., Traversari C;
Db	5041	TTACAGCATCCAAAGTTATGATGACAGACTCACAGTCACAGTCACAGTCAC	5100	PI	Van Den Eynde B., Van Der Bruggen P., Van Pei A;
Db	5041	TTACAGCATCCAAAGTTATGATGACAGACTCACAGTCACAGTCACAGTCAC	5100	DR	WPI: 92-415460/50.
Qy	5101	TAAGAGTCTGTTTATTCAAGATTGGAAATCCATTCTATTGCAATTGGATAAT	5160	PT	Nucleic acid mol: encoding a human tumour rejection antigen precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5101	TAAGAGTCTGTTTATTCAAGATTGGAAATCCATTCTATTGCAATTGGATAAT	5160	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5161	ACACAGGTGGATAAGTACTAGTACAATGAGTGGATAAAATAGATGAGATA	5220	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5161	ACACAGGTGGATAAGTACTAGTACAATGAGTGGATAAAATAGATGAGATA	5220	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5221	AGAACTAAAGAAATAAGAGATAGTCAACTCTGGCTTACCTCACTGAGTT	5280	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5221	AGAACTAAAGAAATAAGAGATAGTCAACTCTGGCTTACCTCACTGAGTT	5280	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5281	ATTTTAAAGATATATGATCATACCTGGATTTCCTGGCTCTTGTGAAATGTAAGAAAT	5340	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5281	ATTTTAAAGATATATGATCATACCTGGATTTCCTGGCTCTTGTGAAATGTAAGAAAT	5340	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5341	TAATCTGTGATAAAGAATCTCCCTGTTACTGGCTCTTCTCCATGACTGAGCA	5400	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5341	TAATCTGTGATAAAGAATCTCCCTGTTACTGGCTCTTCTCCATGACTGAGCA	5400	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5401	TCTGCTTTTGGAAAGGCCCTGGTTAGTAGTGGAGATGCTAAAGGTAAGCTCATAC	5460	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5401	TCTGCTTTTGGAAAGGCCCTGGTTAGTAGTGGAGATGCTAAAGGTAAGCTCATAC	5460	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5461	CCACCCATAGGGTCAGTCTAGGCTGCACTCACGTAATCGAGGTGGCAAGATGTC	5520	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5461	CCACCCATAGGGTCAGTCTAGGCTGCACTCACGTAATCGAGGTGGCAAGATGTC	5520	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5521	CTCTAAAGATGTGAGGAAAGTGAAGAGGGTAGGGTGCTGGGTGAGAGTG	5580	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5521	CTCTAAAGATGTGAGGAAAGTGAAGAGGGTAGGGTGCTGGGTGAGAGTG	5580	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGATTGGCTGGAAACTCGAGTCCTCT	5640	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGATTGGCTGGAAACTCGAGTCCTCT	5640	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Qy	5641	GGGGAGGTGATGTGAAATGATCTGGTGGATCC	5674	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
Db	5641	GGGGAGGTGATGTGAAATGATCTGGTGGATCC	5674	PT	precursor - used as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
RESULT	2				
Q32352					
ID	032352	standard; DNA: 5674 BP.			
AC	32352;				
DT	22-APR-1993	(first entry)			
DE	MAGE-1 nucleic acid				
KW	melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen precursor; MAGE; gene family; ss.				
OS	Homo sapiens.				
FH	Key	Location/Qualifiers			
FT	3881 . 4711				

Db	541	CCCCACTCCAATGCTCACTCCGTGACCCAAACCCCCCTCTTCAATTGTCATTCCAAACCCCCA	600
Qy	601	CCCCACATCCCCAACCCCATCTCCCATGCCCATGCCCTAACCCCTCATGCCCATGCCCATTCACCCCT	660
Db	601	CCCCACATCCCCAACCCCATCTCCCATGCCCATGCCCTAACCCCTCATGCCCATGCCCATTCACCCCT	660
Qy	661	CACCCCCCACCACCCCCACTCCCCAACCCCCAGGATCGGTCTCCG	720
Db	661	CACCCCCCACCACCCCCACTCCCCAACCCCCAGGATCGGTCTCCG	720
Qy	721	CGAGAACATCGGTGCGGCGATGTGACGCCACGACTTGCGATTTGTTGGCAGAGA	780
Db	721	CGAGAACATCGGTGCGGCGATGTGACGCCACGACTTGCGATTTGTTGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCATCTGACCGGACGGCTGAGGTGACCCAGG	840
Db	781	GAAGCGAGGTTTCATCTGACCGGACGGCTGAGGTGACCCAGG	840
Qy	841	CCTCTGAGGGAGCAAGGTGAGGGAGCTGAGGACCCGGCCACTCCAAATA	900
Db	841	CCTCTGAGGGAGCAAGGTGAGGGAGCTGAGGACCCGGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAATATTTCAGCCCCGCCCCCTGGCCACCGGGGAAAGA	960
Db	901	GAGAGCCCCAATATTTCAGCCCCGCCCCCTGGCCACCGGGGAAAGA	960
Qy	961	CCCTCACGCCCTGGCTCCAAAAGCTTGTGAGAACCCAGGTT	1020
Db	961	CCCTCACGCCCTGGCTCCAAAAGCTTGTGAGAACCCAGGTT	1020
Qy	1021	TCTCTCCCCAAGCTCTGGAATCAGAGTTGCTGACCGGGAGGACTGGTTAGGGAGG	1080
Db	1021	TCTCTCCCCAAGCTCTGGAATCAGAGTTGCTGACCGGGAGGACTGGTTAGGGAGG	1080
Qy	1081	GAGGGCACGGCTCGCCAGGATCAGATAGACCCCANAGGAGGTTGGGCC	1140
Db	1081	GAGGGCACGGCTCGCCAGGATCAGATAGACCCCANAGGAGGTTGGGCC	1140
Qy	1141	CCCATCTCTGACTAGACCCCTACCTCCATCTGACCTGACCCAAAC	1200
Db	1141	CCAGACTGACTCCATCTGACCTGACCCAAAC	1200
Qy	1201	CCCATCTCTGACTAGACCCCTACCTCCATCTGACCTGACCCAAAC	1260
Db	1201	CCCATCTCTGACTAGACCCCTACCTCCATCTGACCTGACCCAAAC	1260
Qy	1321	GGTTTGCCTCTCATGTCAGCTACCTCCATGCCCTACTCGGAGATCC	1380
Db	1321	CCACCCCTCATCTCATGTCAGCTACCTCCATGCCCTACTCGGAGATCC	1380
Qy	1381	GGTTTGCCTCTCATGTCAGCTACCTCCATGCCCTACTCGGAGATCC	1440
Db	1381	GGTTTGCCTCTCATGTCAGCTACCTCCATGCCCTACTCGGAGATCC	1440
Qy	1441	TGAACTCTCACAGATCTGAGAGGCCAGGTGTTAATGGTCTAGGGGGCTGAG	1500
Db	1441	TGAACTCTCACAGATCTGAGAGGCCAGGTGTTAATGGTCTAGGGGGCTGAG	1500
Qy	1501	ATCGACTGGGGAGTGTAGGAGCTGTAAGGGAGCTGGTAGGCGATGAAACACTGACT	1560
Db	1501	ATCGACTGGGGAGTGTAGGAGCTGTAAGGGAGCTGGTAGGCGATGAAACACTGACT	1560
Qy	1561	ATCGAGGGGCCACACCCCCAGGTAGTGGCCAAATGATCCACCCCTGCTG	1620
Db	1561	ATCGAGGGGCCACACCCCCAGGTAGTGGCCAAATGATCCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACACCCGGCGAGACAGATGTCAGTGCAGACCCCCGGCTCC	1680
Db	1621	CCAGCCCTGGACACCCGGCGAGACAGATGTCAGTGCAGACCCCCGGCTCC	1680
Qy	1681	CACTGCCAATCTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Db	1681	CACTGCCAATCTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Qy	1741	GCTCAGGAGGAGCAGGCCAGGCTCATCAAGTCCAGCATCGCCCGCAATTAGGGTCAGG	1800
Db	1741	GCTCAGGAGGAGCAGGCCAGGCTCATCAAGTCCAGCATCGCCCGCAATTAGGGTCAGG	1800
Qy	1801	ACCTGGAGGGAAACTTGAGGGTTCCCCACCCACACCTGCTCATCTCCACGCCACC	1860
Db	1801	ACCTGGAGGGAAACTTGAGGGTTCCCCACCCACACCTGCTCATCTCCACGCCACC	1860
Qy	1861	CCACTCACATTCACCATACTACCTCCATACCTCCACACCTCATCTGCAATCCCTGCTG	1920
Db	1861	CCACTCACATTCACCATACTACCTCCATACCTCCACACCTCATCTGCAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAAGCCACGGGAATGGGCCAGGACTCGGATCTGACGTCCCCATCA	1980
Db	1921	TCAACCCACGGAAAGCCACGGGAATGGGCCAGGACTCGGATCTGACGTCCCCATCA	1980
Qy	1981	GGGTCATGGAGGGAAAGGGCTCTGACAGGGCCTAGGGAGCAGGGAGGGCCCTAC	2040
Db	1981	GGGTCATGGAGGGAAAGGGCTCTGACAGGGCCTAGGGAGCAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGGGCTCAGAGGACCCAGGACCCCTAGGACCCACCCCTGTCAG	2100
Db	2041	TGCGAGATGAGGGGGCTCAGAGGACCCAGGACCCACCCCTGTCAG	2100
Qy	2101	ACTGAGGCTTGCCACTCTGGCTCATGAGATGGGGACTCATGTCAGTGGGG	2160
Db	2101	ACTGAGGCTTGCCACTCTGGCTCATGAGATGGGGACTCATGTCAGTGGGG	2160
Qy	2161	GTGGGACCCAGGGCTCAGGGAGGCTGAGGACCCAGGACCCAGGACCTGTCAG	2220
Db	2161	GTGGGACCCAGGGCTCAGGGAGGCTGAGGACCCAGGACCCAGGACCTGTCAG	2220
Qy	2221	GGATCCAGATAGTGTGACCTGGCCCTAGAGTGGGGACTCAGGGACGGTGGCCACATA	2280
Db	2221	GGATCCAGATAGTGTGACCTGGCCCTAGAGTGGGGACTCAGGGACGGTGGCCACATA	2280
Qy	2281	GCCCCATTTCCTGCACTTGTGAGGTGACAGGACAGCTGGTGTGAGAAGTGGGG	2340
Db	2281	GCCCCATTTCCTGCACTTGTGAGGTGACAGGACAGCTGGTGTGAGAAGTGGGG	2340
Qy	2341	TCAAGTGGGATATCCCGGGCTCAGAGTGGGTGACAGCTGGTGTGAGAAGTGGGG	2400
Db	2341	TCAAGTGGGATATCCCGGGCTCAGAGTGGGTGACAGCTGGTGTGAGAAGTGGGG	2400
Qy	2401	TTAGTACCTCTAGGGGACCCAGATCAGGATGTCGGTCACTTGTCAG	2460
Db	2401	TTAGTACCTCTAGGGGACCCAGATCAGGATGTCGGTCACTTGTCAG	2460
Qy	2461	ACTCATGTCAGGGAAATGGGGTGTGAGGAGCTGTCATCTGTCAG	2520
Db	2461	TTAGTACCTCTAGGGGACCCAGATCAGGATGTCGGTCACTTGTCAG	2520
Qy	2521	CAGGCAGGAATTTGGGGTGTGGAGATCCACACCCAGAACCAAAGGGGTCT	2580
Db	2521	CAGGCAGGAATTTGGGGTGTGGAGATCCACACCCAGAACCAAAGGGGTCT	2580
Qy	2581	GGACACAGAACGGCTATTGGATTCACCCAGAACCAAAGGGGTCACTGTCAG	2640
Db	2581	ACTCATGTCAGGGAAATGGGGTGTGGAGATCCACACCCAGAACCAAAGGGGTCACTGTCAG	2640
Qy	2641	GAGACACAGAACGGCTATTGGATTCACCCAGAACCAAAGGGGTCACTGTCAG	2700
Db	2641	GAGACACAGAACGGCTATTGGATTCACCCAGAACCAAAGGGGTCACTGTCAG	2700
Qy	2701	TCACCCAGATUTGGCTCTTCTACTCCCTGTTCCAGAATCTGGGAGGGACT	2760
Db	2701	TCACCCAGATUTGGCTCTTCTACTCCCTGTTCCAGAATCTGGGAGGGACT	2760

Qy	2761	CATTCTAGAGGGTGAATCAGGTAACTGAGGCCCATCTGGCTTAAGACAGAGCG	2820
Db	2761	CATTCTAGAGGGTGAATCAGGTAACTGAGGCCCATCTGGCTTAAGACAGAGCG	2820
Qy	2821	GTCAGGATCTGCATGGTCAAGGAGACTGAGAACATGGGGAGCTGAGGTACCCAG	2880
Db	2821	GTCAGGATCTGCATGGTCAAGGAGACTGAGAACATGGGGAGCTGAGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGAGACTGCACAGAAATCACCCCTGCCCTGGTTGAGGAACATGGGGAGCTGAGGTACCCAG	2940
Db	2881	GACCAGAACACTGAGGAGACTGCACAGAAATCACCCCTGCCCTGGTTGAGGTACCCAG	2940
Qy	2941	AGCATGGCTGGCCGCTTGCCGAGGTCTCTTCGTTATCCTGGACATGATGTAGGG	3000
Db	2941	AGCATGGCTGGCCGCTTGCCGAGGTCTCTTCGTTATCCTGGACATGATGTAGGG	3000
Qy	3001	ACGGGAGGCGCTTGGTCAAGGAGGACCTCACCCAGGACATCTAAATTCCAAAT	3060
Db	3001	ACGGGAGGCGCTTGGTCAAGGAGGACCTCACCCAGGACATCTAAATTCCAAAT	3060
Qy	3061	CTGCCAGGAGTCAGGTGAGGACCAAGGGGGCACCTCACCCAGGACATCTAAATTCCAAAT	3120
Db	3061	CTGCCAGGAGTCAGGTGAGGACCAAGGGGGCACCTCACCCAGGACATCTAAATTCCAAAT	3120
Qy	3121	GAATTGATATCTCTGCTGCCCTTCCCAAGGACCTAGGCACGTGTCAGGTT	3180
Db	3121	GAATTGATATCTCTGCTGCCCTTCCCAAGGACCTAGGCACGTGTCAGGTT	3180
Qy	3181	GTCCTCTTCCGTCCTCCATCTCCATCTCCATCTGGATGAACTCTGATTTGGATTTCTCAG	3240
Db	3181	GTCCTCTTCCGTCCTCCATCTCCATCTGGATGAACTCTGATTTGGATTTCTCAG	3240
Qy	3241	ACCGCAAAAGGGCAGGATCCAGGCCCTGCGAGAAAATAAAGGCCCTGCGTAGAAA	3300
Db	3241	ACCGCAAAAGGGCAGGATCCAGGCCCTGCGAGAAAATAAAGGCCCTGCGTAGAAA	3300
Qy	3301	CAGAGGGTCACTCACCTGATGAGTGGGAGCTCACAGAGTCAGGCCCTCTG	3360
Db	3301	CAGAGGGTCACTCACCTGATGAGTGGGAGCTCACAGAGTCAGGCCCTCTG	3360
Qy	3361	GTAAGCATCTGAGAAGCCAGGCTGTCTGGGTCTGACCCCTGAGGCCCTGGATTCCT	3420
Db	3361	GTAAGCATCTGAGAAGCCAGGCTGTCTGGGTCTGACCCCTGAGGCCCTGGATTCCT	3420
Qy	3421	CITCCCTGGCTCCAGAACCCAGGAGCTGGCTGTGAGAACAGTATCCTCTAGGTC	3480
Db	3421	CITCCCTGGCTCCAGAACCCAGGAGCTGGCTGTGAGAACAGTATCCTCTAGGTC	3480
Qy	3481	ACAGAGGGAGGGATGCAAGGGTGTGCCAGCAGTCAGTGTGGCTTAAGTCACCAA	3540
Db	3481	ACAGAGGGAGGGATGCAAGGGTGTGCCAGCAGTCAGTGTGGCTTAAGTCACCAA	3540
Qy	3541	GGCCCCACCTGCCAACACATGGACTCCAGAACAGTCGGCTCACCTCCPACTG	3600
Db	3541	GGCCCCACCTGCCAACACATGGACTCCAGAACAGTCGGCTCACCTCCPACTG	3600
Qy	3601	TCACTCTGTAGATCTGACCTCTGTCGGGGCTGACCCCTGAGTCAGTTCTC	3660
Db	3601	TCACTCTGTAGATCTGACCTCTGTCGGGGCTGACCCCTGAGTCAGTTCTC	3660
Qy	3661	CCTTCAGGTTTCAAGGGACAGGGCAACCCAGAGCAAGGATTTCTGGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTCAAGGGACAGGGCAACCCAGAGCAAGGATTTCTGGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAACTGTAGATGGCTTGTAGTCAGGTTCAAGGTTCACTTC	3780
Db	3721	GAGCACCAAGGAGAACTGTAGATGGCTTGTAGTCAGGTTCAAGGTTCACTTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTGCCCTGCTGCCAGCTTCATGGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTGCCCTGCTGCCAGCTTCATGGCCAGCT	3840

Db	4921	GAAGAGAGGGTCAGTGTCTCACTAGTAGTTCTGTTATGGTGACTGGAGATT	4980	PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT, Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
Qy	4981	TATCTTTGTTCTCTTTGGATTTGTTCAATGTTTTTAAGGATGGTTGATGAA	5040	PI Stockert E, Van der Bruggen P;
Db	4981	TATCTTTGTTCTCTTTGGATTTGTTCAATGTTTTAAGGATGGTTGATGAA	5040	DR WPI : 95-283606/37.
Qy	5041	TTACGCACTCCAAAGTTATGATGACAGACTCACAGTCTGTSTATATAGTTAAGGG	5100	PT New monoclonal antibody binding specifically to MAGE-1 - useful for diagnosis and monitoring of cancer, also new hybridomas, recombinant MAGE-1 and immunogenic peptide(s).
Db	5041	TTACGCACTCCAAAGTTATGATGACAGACTCACAGTCTGTSTATATAGTTAAGGG	5100	PT Disclosure: Page 16-19; 33pp; English.
Qy	5101	TAAGACTCTTGTCTTTATTCAAGATGGAAATCCATTCTATTGTGAATTGGATAAT	5160	CC A monoclonal antibody directed against the tumour rejection antigen (MAGE-1) can be used to detect MAGE-1 in samples by standard immunosassay methods for diagnosis and monitoring of cancer etc. The monoclonal antibody is designated MA454 and is produced by the hybridoma deposited as ATCC HBB11540. The monoclonal antibody is specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
Db	5101	TAAGACTCTTGTCTTTATTCAAGATGGAAATCCATTCTATTGTGAATTGGATAAT	5160	CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as immunogens for production of the monoclonal antibody and antisera.
Qy	5161	AACACCGTGGATAAGTACTTAAATGAGCTAAATGAGATAAGTAGATAAA	5220	CC Sequence 5724 , BP; 1282 A;
Db	5161	AACACCGTGGATAAGTACTTAAATGAGCTAAATGAGATAAGTAGATAAA	5220	CC Sequence 1589 G; 1653 C;
Qy	5221	AGAACTAAAGAAATAAGAGATAGTCAACTCTGCTTATACTCTAGTCTATTCGTA	5280	DB 1; Length 5724;
Db	5221	AGAACTAAAGAAATAAGAGATAGTCAACTCTGCTTATACTCTAGTCTATTCGTA	5280	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	5281	ATTTTTAACATATATGCTACACCTCGGATTCTCTGGCTCTTCTGAAATGTAAGAAAT	5340	Qy 1 CCGGGGCCACACTGGCATCTCCCTTACCCCAATCCCTTACGCACCC 60
Db	5281	ATTTTTAACATATATGCTACACCTCGGATTCTCTGGCTCTTCTGAAATGTAAGAAAT	5340	Db 1 CCGGGGCCACACTGGCATCTCCCTTACCCCAATCCCTTACGCACCC 60
Qy	5341	TAATCTGTAAAGAAATCTCTGGTCACTGGCTCTTCTCTGGCTCTTCTGAAATGTAAGAAAT	5400	Qy 61 ATCCAAACATCTTACGCTACCCCAAGGCCAAAGGCCAAATCCGTTCCACCCCTG 120
Db	5341	TAATCTGTAAAGAAATCTCTGGTCACTGGCTCTTCTCTGGCTCTTCTGAAATGTAAGAAAT	5400	Db 61 ATCCAAACATCTTACGCTACCCCAAGGCCAAATCCGTTCCACCCCTG 120
Qy	5401	TCTCGCTTTGGAAAGGCCCTGGTTAGTAGTGAGATGCTAAAGTAAGCAGCTCATAC	5460	Qy 121 CTCTAACACCCAGGGAGGCCAGGCTCCACATGTCACGCCACTGACTGTGCAATTAGTG 180
Db	5401	TCTCGCTTTGGAAAGGCCCTGGTTAGTAGTGAGATGCTAAAGTAAGCAGCTCATAC	5460	Db 121 CTCTAACACCCAGGGAGGCCAGGCTCCACATGTCACGCCACTGACTGTGCAATTAGTG 180
Qy	5461	CCACCCATAGGGTCTGCTAGACTCTAGGACTCTCACGTAATCGAGGTTGCCAGATGTC	5520	Qy 181 TTAGAGAAGNGGAGTTTCGGTCTGAGGGCTTGGATCTGGAGGGAAAGGG 240
Db	5461	CCACCCATAGGGTCTGCTAGACTCTAGGCTCACGTCAGTCACTGAGGTGGCAAGATGTC	5520	Db 181 TTAGAGAAGNGGAGTTTCGGTCTGAGGGCTTGGATCTGGAGGGAAAGGG 240
Qy	5521	CTCTAAAGATGAGCTAAAGTGAAGGGTAGGCTGGCTCCGGTAGAGT	5580	Qy 241 CCCAGCTCTTAAGAGGCAAGGTGACATCTGAGGGAGACTGAGGCCACATCTGGCTGGACTCT 360
Db	5521	CTCTAAAGATGAGCTAAAGTGAAGGGTAGGCTGGCTCCGGTAGAGT	5580	Db 301 AGATAGAGGCCAAATAATCCCTCATGCCAGCTGCTGAGCTGGCTGACTCT 360
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGCAATTGGCTTTGGAAACTCGAGTTCTCT	5640	Qy 361 TCAGGCTGGCCACCCCCAGCCCTTGTGCTTAACACACTGGGACTCTGAACTCAGAG 420
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGCAATTGGCTTTGGGACTGGCTCT	5640	Db 361 TCAGGCTGGCCACCCCCAGCCCTTGTGCTTAACACACTGGGACTCTGAACTCAGAG 420
Qy	5641	GGGGAGCTGATGTAAATGCTGCTGGTGGATCC	5674	Qy 421 CTCCGCTGATCAGGGAGGGCTGCTTGGAGAGGGCAGCTCCAGGCAAGACAT 480
Db	5641	GGGGAGCTGATGTAAATGCTGCTGGTGGATCC	5674	Db 421 CTCCGCTGATCAGGGAGGGCTGCTTGGAGAGGGCAGCTCCAGGCAAGACAT 480
Key				Qy 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCTCCCTAAGGCCCAACTCCGTGACCAAC 540
Location/Qualifiers				Db 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCTCCCTAAGGCCCAACTCCGTGACCAAC 540
FT	3881 . 4711			Qy 541 CCCACTCCTAGTCAGTCACTCCCTGACCCAAACCCCTCTCATGTCATCCACCCCA 600
/tag=	a			Db 541 CCCACTCCTAGTCAGTCACTCCCTGACCCAAACCCCTCTCATGTCATCCACCCCA 600
/product=	Tumour rejection antigen MAGE-1.			Qy 661 CACCCCCACCCACCCCCACCCCCACCTCCACCCCACTCCGCTGGTCCCG 720
/note=	"The CDS is not indicated in the text of the specification but is suggested in the layout of the sequence."			Dh 661 CACCCCCACCCACCCCCACCCCCACCTCCACCCCACTCCGCTGGTCCCG 720
PN	W09520974-A1.			Qy 721 CCAGGAAACATCATGGCTGGCTGGGGATGTAAGCTGAGCTGTCATGTCATCCACCCCA 600
PD	10-AUG-1995.			
PF	05-JAN-1995; U00095.			
PR	01-FEB-1994; US-190411.			
PA	(LUDWIG INST CANCER RES.			
PA	SLOAN KETTERING INST CANCER RES.			

Db	721	CCAGGAAACATCCGGGTGCCGATGTGACGCCACTGACTTGGCATTGTGGCAGAGA	780
Qy	781	GAAGCAGATTTCATTTCTGAGGCAGCGTAGTTCGGCCAGAACCTGACCG	840
Db	781	GAAGCAGATTTCATTTCTGAGGCAGCGTAGTTCGGCCAGAACCTGACCG	840
Qy	841	CCTGTGAGGGCAAGGTGAGGGCTAGGGGACTGAGGACCCGCCACTCCAATA	900
Db	841	CCTGTGAGGGCAAGGTGAGGGCTAGGGGACTGAGGACCCGCCACTCCAATA	900
Qy	901	GAGAGCCCCAAATTTCAGCCCCCTTGCGCACCCCTGGCCACCCGGGAGA	960
Db	901	GAGAGCCCCAAATTTCAGCCCCCTTGCGCACCCCTGGCCACCCGGGAGA	960
Qy	961	CTCTCCCCAAAGCTGGATCATGGAGCTGGAGGACTGAGGCCCGCCACTCCAATA	1020
Db	961	CTCTCCCCAAAGCTGGATCATGGAGCTGGAGGACTGAGGCCCGCCACTCCAATA	1020
Qy	1021	TTCCTCCCCAAAGCTGGATCATGGAGCTGGAGGACTGGTAGGAGAGG	1080
Db	1021	TTCCTCCCCAAAGCTGGATCATGGAGCTGGAGGACTGGTAGGAGAGG	1080
Qy	1081	GCAGGGCAGCGCTGGCTGGCCAGGGATCAAGATCGACGGGAGCTGGTAGGAGG	1140
Db	1081	GCAGGGCAGCGCTGGCTGGCCAGGGATCAAGATCGACGGGAGCTGGTAGGAGG	1140
Qy	1141	CCAGACTGCACTCCAATCCCATTCCCTACCTCCATCCACCCAAAC	1200
Db	1141	CCAGACTGCACTCCAATCCCATTCCCTACCTCCATCCACCCAAAC	1200
Qy	1201	CCCATCTCTCAGCTACACCTCACCCTACTCCCTACTCCCTACCTGACCAAC	1260
Db	1201	CCCATCTCTCAGCTACACCTCACCCTACTCCCTACTCCCTACCTGACCAAC	1260
Qy	1261	ACCTCTCCAGCCACCCAGCACCGCCCAACCCCTTGCCACCTACCTGCCAAC	1320
Db	1261	ACCTCTCCAGCCACCCAGCACCGCCCAACCCCTTGCCACCTACCTGCCAAC	1320
Qy	1321	CCACCCCTCATCTCATGTCCTCCACCTCCATCCACCCCAACTCCATCCGACACC	1380
Db	1321	CCACCCCTCATCTCATGTCCTCCACCTCCATCCACCCCAACTCCATCCGACACC	1380
Qy	1381	GGTTTGCCTCTGCTCTCACCCAGGGCTGTAGCCCATGTGAAACCACTACT	1440
Db	1381	GGTTTGCCTCTGCTCTCACCCAGGGCTGTAGCCCATGTGAAACCACTACT	1440
Qy	1441	TGAACCTCACAGTCTGAGAAGCCAGGTTCTGGTGTAGCTGGCTGAG	1500
Db	1441	TGAACCTCACAGTCTGAGAAGCCAGGTTCTGGTGTAGCTGGCTGAG	1500
Qy	1501	ATCCACTGAGGACACCCCAAGTGTAGCCAAATGTACAGTACCCCTCTG	1620
Db	1501	ATCCACTGAGGACACCCCAAGTGTAGCCAAATGTACAGTACCCCTCTG	1620
Qy	1561	ACTGAGGGACACCCCAAGTGTAGCCAAATGTACAGTACCCCTCTG	1620
Db	1561	ACTGAGGGACACCCCAAGTGTAGCCAAATGTACAGTACCCCTCTG	1620
Qy	1621	CCAGCCCTGGACCAACCCGGCCAGGACACATCTCAGTGGACACCCCTCC	1680
Db	1621	CCAGCCCTGGACCAACCCGGCCAGGACACATCTCAGTGGACACCCCTCC	1680
Qy	1681	CACTGCCACTAACCCAGGGAAATCTGAGCTGAGCTGAGCTGGCTGAG	1740
Db	1681	CACTGCCACTAACCCAGGGAAATCTGAGCTGAGCTGAGCTGGCTGAG	1740
Qy	1741	GGTCAAGGAGGCCAGGGCCAGGCACTAACCCAGGGAAATCTGAGCTGG	1800
Db	1741	GGTCAAGGAGGCCAGGGCCAGGCACTAACCCAGGGAAATCTGAGCTGG	1800
Qy	1801	ACCTGGGAGGGAACTGAGGGTCCCAACCCACCCAGGGCACC	1860
Db	1801	ACCTGGGAGGGAACTGAGGGTCCCAACCCACCCAGGGCACC	1860

Qy	3376	CAGGGCTGTGGTCTGCCACCTGAGGGCCCTGGATTCTCTGGACCTCA	3435
Db	121	CAGGGCTGTGGTCTGCCACCTGAGGGCCCTGGATTCTCTGGACCTCA	180
Qy	3436	GGAAACCGGCACTGAGGCCCTGGCTCAGAGCACAGGATG	3495
Db	181	GGAAACCGGCACTGAGGCCCTGGCTCAGAGCACAGGATG	240
Qy	3496	CAACGGGTGTGCCACAGGTGAATGTTGCCCTGAATGCCACACCAAGGGCCCCAACCTGCCA	3555
Db	241	CAACGGGTGTGCCACAGGTGAATGTTGCCCTGAATGCCACACCAAGGGCCCCAACCTGCCA	300
Qy	3556	CAAGGACATAGACTCCACAGGTGTGGCTGAGTACCCCTCTCAGCTTCAGGTTTCAG	3615
Db	301	CAAGGACATAGACTCCACAGGTGTGGCTGAGTACCCCTCTCAGCTTCAGGTTTCAG	360
Qy	3616	CGACCCCTGTGGCCGGCTGAGTACCCCTCTCAGCTTCAGGTTTCAG	3675
Db	361	CGACCCCTGTGGCCGGCTGAGTACCCCTCTCAGCTTCAGGTTTCAG	420
Qy	3676	GGACAGGCCAACCCAGAGACAGGATTCCCTGGGGCCACAGAGGACCCAAGGAGA	3735
Db	421	GGACAGGCCAACCCAGAGACAGGATTCCCTGGGGCCACAGAGGACCCAAGGAGA	480
Qy	3736	GATCCTGAATGAGGCTTGTAGCTCAAGGTTCAAGTTCTCAGCTGGGCTCTCA	3795
Db	481	GATCCTGAATGAGGCTTGTAGCTCAAGGTTCAAGTTCTCAGCTGGGCTCTCA	540
Qy	3796	CACACTCCCCTCTCCCCAGGCCCTGGCTCTCATGGCCACACTCT	3855
Db	541	CACACTCCCCTCTCCCCAGGCCCTGGCTCTCATGGCCACACTCT	600
Qy	3856	GCCTGTGCCCTGAGGAGTCATATGTCCTCTAGCAGGAGGTCGACTGAAAGCC	3915
Db	601	GCCTGTGCCCTGAGGAGTCATATGTCCTCTAGCAGGAGGTCGACTGAAAGCC	660
Qy	3916	TGAGGAGGCCAACAGGCCCTGGCTCTGGAGGGCTGCCAC	3975
Db	661	TGAGGAGGCCAACAGGCCCTGGCTCTGGAGGGCTGCCAC	720
Qy	3976	CTCCPCTCTCTCTGCTGGCACCTCTGCTCTGGAGGGCTGCCACAGCTGGCTCA	4035
Db	721	CTCCPCTCTCTCTGCTGGCACCTCTGCTCTGGAGGGCTGCCAC	780
Qy	4036	AGATCTCCCCAGAGTCCTAGGGACCTGGCCCTTCCACTACATCACTCAG	4095
Db	781	AGATCTCCCCAGAGTCCTAGGGACCTGGCCCTTCCACTACATCACTCAG	840
Qy	4096	ACAGAGGCAACCCAGTCGGCTTCAAGCAGCCGAGGAGGGCCAGACCTCTG	4155
Db	841	ACAGAGGCAACCCAGTCGGCTTCAAGCAGCCGAGGAGGGCCAGACCTCTG	900
Qy	4156	TATCCGGAGCTCTGGCATGTCGGAGCTAACACTAACAGAGCTGGCTCTG	4215
Db	901	TATCCGGAGCTCTGGCATGTCGGAGCTAACACTAACAGAGCTGGCTCTG	960
Qy	4216	TCTGTCCTCAAATATGAGGCCAGTCAGTCAGAACATGGGAGAGTGT	4275
Db	1021	TCTGTCCTCAAATATGAGGCCAGTCAGTCAGAACATGGGAGAGTGT	1080
Qy	4336	GCTGGGCTCTGGCATGTCAGTCAGGAGACCCACGGGCACTCTAGTCCTG	4395
Db	1081	GCTGGGCTCTGGCATGTCAGTCAGGAGACCCACGGGCACTCTAGTCCTG	1140
Qy	4396	CACCGCTCTAGTCAGTCAGTCAGTCAGTCAGTAATCAAGATCATGCCAAGAC	4455
Db	1141	CACCGCTCTAGTCAGTCAGTCAGTCAGTCAGTAATCAAGATCATGCCAAGAC	1200

	Query Match	Score	Length	Pred.	No.	Gaps	0;
	Best Local Similarity	42.6%	2415.8;	DB 1;	Length	2419;	
	Matches 241;	Conservative	99.9%;	0;	Mismatches	2;	Indels
o	3226	GGATCCAGGCCCTGCCAGAAAATAATAGGCCCTGCCGAGAACAGGGGGCATCC	3315				
	1	GGATCCAGGCCCTGCCAGAAAATAATAGGCCCTGCCGAGAACAGGGGGCATCC	60				
o	3316	ACGTGATGAGTGGATGGATGCAAGAGTCAGCCACCTCTGTAGACTGAAAGC	3375				
	61	ACGTGATGAGTGGATGGATGCAAGAGTCAGCCACCTCTGTAGACTGAAAGC	120				
o	3376	CAGGGCTGTCTCGCAGCTGACCCCTGCCAGAGTCAGCCACCTCTGTAGACTGAAAGC	3435				
	121	CAGGGCTGTCTCGCAGCTGACCCCTGCCAGAGTCAGCCACCTCTGTAGACTGAAAGC	180				
o	3436	GAACACCAGCAGCAGGCCCTGGCTGAAACATCCAGCTGAAAGCAGGGATG	3495				
	181	GAACACCAGCAGCAGGCCCTGGCTGAAACATCCAGCTGAAAGCAGGGATG	240				
o	3496	CACAGGCTGTCTGCCAGCTGAAATGGCTGAACTGCAACANGGCCACCTGCCA	3555				
	241	CACAGGCTGTCTGCCAGCTGAAATGGCTGAACTGCAACANGGCCACCTGCCA	300				
o	3556	CAGGACACATAGGACTCCAGACTGCTGGCTCTACTCTAGCTGTAGAAAT	3615				
	301	CAGGACACATAGGACTCCAGACTGCTGGCTCTACTCTAGCTGTAGAAAT	360				
o	3616	CAGGACACATAGGACTCCAGACTGCTGGCTCTACTCTAGCTGTAGAAAT	3675				
Dh	1441	GAAACCAGCTATGTGAAGTCCTGTAGTGTGCAAGTGTCAAGTGTGCTTT	4755				
Db	361-	CGACCTCTTGCGCTGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCTTCAATG	4 20				
Qy	2281	AAAAAGTGAGAGAGGGTAGGGGTAGGGCTCGGGTAGGGTAGGGTAGGT	2340				
Db	5596	CTGACCTGGGATATTGGCTGGAAACCTGGAGTCTTCGGGGAGCAGATGT	5655				
Db	2341	CTCTGAGCTGGGATTTGGCTGGATCTGGAAACCTGGAGCTCTGGCTGATGT	2400				
Qy	5656	ATGATCTTGGTGATCC 5674					
Db	2401	ATGATCTTGGTGATCC 2419					
	RESULT	6					
	5086	T05086 standard; DNA: 2419 BP.					
	TO-086;	26-FEB-1996 (first entry)					
	M2-MEL	melanoma; M2-MEL; tumour rejection antigen; cancer; diagnosis; ss.					
	Homo sapiens.						
	W0952387-A1.						
	08-SEP-1995.						
	23-FEB-1995.						
	01-MAR-1994;	002203.					
	10-MAR-1994;	US-204172.					
	10-SEP-1994;	US-209172.					
	30-NOV-1994;	US-298849.					
	(LUDW-) LUDWIG INST CANCER RBS.	336774.					
	Boon-Falleur T., Brasseur F., Chomez P., De Plaein E;						
	De Smet C., Gauger B., Lethe B., Marchand M., Patard J;						
	Szikora J., van den Eynde B., Van Derbruggen P., Weynants P;						
	WPI: 95-320516/41.						
	Determination of cancerous condition(s) - using a nucleic acid as a primer to determine expression of a MAGE tumour rejection antigen precursor.						
	Example 20; Page 69-70; 121pp; English.						
	A gene sequence (105086) hybridizes with a 2.4 kb fragment from human melanoma cell line MZ2-MEL but not with E- antigen loss variants of MZ2-MEL. This E precursor antigen gene sequence was obtd. from a cosmid derived from DNA of the E+ subclone MZ2-MEL 4.3. Sequence 2419 BP; 560 A; 581 C; 677 G; 601 T;						
	Query Match	42.6%	Score 2415.8;	DB 1;	Length 2419;		
	Best Local Similarity	99.9%;	Pred. No. 0;	0;	Mismatches	0;	
	Matches 241;	Conservative	0;				
o	3226	GGATCCAGGCCCTGCCAGAAAATAATAGGCCCTGCCGAGAACAGGGGGCATCC	3315				
	1	GGATCCAGGCCCTGCCAGAAAATAATAGGCCCTGCCGAGAACAGGGGGCATCC	60				
o	3316	ACGTGATGAGTGGATGGATGCAAGAGTCAGCCACCTCTGTAGACTGAAAGC	3375				
	61	ACGTGATGAGTGGATGGATGCAAGAGTCAGCCACCTCTGTAGACTGAAAGC	120				
o	3376	CAGGGCTGTCTCGCAGCTGACCCCTGCCAGAGTCAGCCACCTCTGTAGACTGAAAGC	3435				
	121	CAGGGCTGTCTCGCAGCTGACCCCTGCCAGAGTCAGCCACCTCTGTAGACTGAAAGC	180				
o	3436	GAACACCAGCAGCAGGCCCTGGCTGAAACATCCAGCTGAAAGCAGGGATG	3495				
	181	GAACACCAGCAGCAGGCCCTGGCTGAAACATCCAGCTGAAAGCAGGGATG	240				
o	3496	CACAGGCTGTCTGCCAGCTGAAATGGCTGAACTGCAACANGGCCACCTGCCA	3555				
	241	CACAGGCTGTCTGCCAGCTGAAATGGCTGAACTGCAACANGGCCACCTGCCA	300				
o	3556	CAGGACACATAGGACTCCAGACTGCTGGCTCTACTCTAGCTGTAGAAAT	3615				
	301	CAGGACACATAGGACTCCAGACTGCTGGCTCTACTCTAGCTGTAGAAAT	360				
o	3616	CAGGACACATAGGACTCCAGACTGCTGGCTCTACTCTAGCTGTAGAAAT	3675				
Dh	1441	GAAACCAGCTATGTGAAGTCCTGTAGTGTGCAAGTGTCAAGTGTGCTTT	4755				

QY	4756	TTCCTCCATCTCGTGAACGAGCTTGTAGAGAGGGACTTGAGAGGAGCTGAGCATGA	4815	KW cancer; cytolytic T cells; antigen D; human leucocyte antigen: ss.
OS		Homo sapiens.		
PN		W0942031-A.		
PD		13-OCT-1994.		
PF		17-MAR-1994;		
PR		002877.		
PA		(LUDW-) LUDWIG INST CANCER RES.		
PI		Boon-falleur T.; Gaugier B., Van DER BRUGGEN P;		
DR		WPI: 94-333192/41.		
PT		New tumour rejection antigen precursor MAGE3 - useful in treatment and diagnosis of cancer		
PS		Example 20, Page 28, 105pp, English.		
CC		Q72472 is the tumour rejection antigen E precursor gene, another gene Q72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection antigen precursor. Melanoma characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytotoxic T cells specific for the complex of antigen D (the mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).		
CC		Sequence 2420 BP; 562 A;	582 C;	677 G;
CC		599 T;		
SQ				
Query Match		-42.4%; Score 2408; DB 1; Length 2420;		
Best Local Similarity		.10.0%.	Pred. No. 0;	
Matches		Conservative 0; Mismatches 0; Indels 1; Gaps 1		
Matches	2419;			
QY	4936	TGTTCTCACTAGTAGGTTCTCTCTATGGGACTTGAGATTATCTTGTCTCT 4995		
QY	1561	GTTCAGGCAAAGGCACAGTGGGACTTGGCCATCTGGCTGAAGCAGCTTGTGATGA	1560	
DDB		1561 GTTCAGGCAAAGGCACAGTGGGACTTGGCCATCTGGCTGAAGCAGCTTGTGATGA	1620	
QY	4876	GCAGCTTCCCCTGCCCTCGCTCGTGTGACATGAGGGCTCGTCACTCTGAGCTGTCAG	4935	
QY	1621	GCAGCTTCCCCTGCCCTCGCTCGTGTGACATGAGGGCTCGTCACTCTGAGCTGTCAG	1680	
Db		1621 GCAGCTTCCCCTGCCCTCGCTCGTGTGACATGAGGGCTCGTCACTCTGAGCTGTCAG		
QY	4936	TGTTCTCACTAGTAGGTTCTCTCTATGGGACTTGAGATTATCTTGTCTCT 4995		
QY	1681	TGTTCTCACTAGTAGGTTCTCTATGGGACTTGAGATTATCTTGTCTCT 1740		
DDB		1681 TGTTCTCACTAGTAGGTTCTCTATGGGACTTGAGATTATCTTGTCTCT 1740		
QY	4996	TGGAAATGTTCAAATGTTTTAAGGGATGGTGAATGAACTCAGCATCAAGT 5055		
QY	1741	TGGAAATGTTCAAATGTTTTAAGGGATGGTGAATGAACTCAGCATCAAGT 1800		
DDB		1741 TGGAAATGTTCAAATGTTTTAAGGGATGGTGAATGAACTCAGCATCAAGT 1800		
QY	5056	TAGTAATGACAGCAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTGTGT 5115		
Db		5056 TAGTAATGACAGCAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTGTGT 5115		
QY	1801	TAGTAATGACAGCAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTGTGT 1860		
QY	5116	TTATTCAATTGGAAATCCATTATTTGTTGATTTGGATAAACAGCATGGATAA 5175		
DDB		5116 TTATTCAATTGGAAATCCATTATTTGTTGATTTGGATAAACAGCATGGATAA 5175		
QY	1861	TTATTCAATTGGAAATCCATTATTTGTTGATTTGGATAAACAGCATGGATAA 1920		
DDB		1861 TTATTCAATTGGAAATCCATTATTTGTTGATTTGGATAAACAGCATGGATAA 1920		
QY	5176	AGTACTTGGAAATGTTGAAATGGCAGTAAATTGGCAGTAAATGGAAATT 5235		
DDB		5176 AGTACTTGGAAATGTTGAAATGGCAGTAAATTGGCAGTAAATGGAAATT 5235		
QY	1921	AGTACTTGGAAATGTTGAAATGGCAGTAAATTGGCAGTAAATGGAAATT 1980		
DDB		1921 AGTACTTGGAAATGTTGAAATGGCAGTAAATTGGCAGTAAATGGAAATT 1980		
QY	5236	AAGAGATAGTAAATTCTGCTTACCTCTGCTTACCTCTGCTTACCTCTG 5295		
DDB		5236 AAGAGATAGTAAATTCTGCTTACCTCTGCTTACCTCTGCTTACCTCTG 5295		
QY	1981	ARGAGATGTCATTCATTCGCTTACCTCTGCTTACCTCTGCTTACCTCTG 2040		
DDB		1981 ARGAGATGTCATTCATTCGCTTACCTCTGCTTACCTCTGCTTACCTCTG 2040		
QY	5296	TGCAATACCTGGATTCCTTGGCTTCTTGGATGAAATGTAAGAAATTCTGAATAAG 5355		
DDB		5296 TGCAATACCTGGATTCCTTGGCTTCTTGGATGAAATGTAAGAAATTCTGAATAAG 5355		
QY	2041	TGATACCTGGATTCCTTGGCTTCTTGGATGAAATGTAAGAAATTCTGAATAAG 2100		
DDB		2041 TGATACCTGGATTCCTTGGCTTCTTGGATGAAATGTAAGAAATTCTGAATAAG 2100		
QY	5356	AACTCTTCTGTCACTGGCTTCTCTCATGGACTCTGGCTTCTCTGGAG 5415		
DDB		5356 AAATCTTCTGTCACTGGCTTCTCTCATGGACTCTGGCTTCTCTGGAG 5415		
QY	2101	AAATCTTCTGTCACTGGCTTCTCTCATGGACTCTGGCTTCTCTGGAG 2160		
DDB		2101 AAATCTTCTGTCACTGGCTTCTCTCATGGACTCTGGCTTCTCTGGAG 2160		
QY	5416	GCCCTGGGTAGTGTGGAGATGTTAGGTAAGCTGAGCTCATACCCATAGGTG 5475		
DDB		5416 GCCCTGGGTAGTGTGGAGATGTTAGGTAAGCTGAGCTCATACCCATAGGTG 5475		
QY	2161	GCCCTGGGTAGTGTGGAGATGTTAGGTAAGCTGAGCTCATACCCATAGGTG 2220		
DDB		2161 GCCCTGGGTAGTGTGGAGATGTTAGGTAAGCTGAGCTCATACCCATAGGTG 2220		
QY	5476	TAGAGCTTGGACTCTGCACGTTAACTGAGGCTCCTCTGAGATGTTAGG 5535		
DDB		5476 TAGAGCTTGGACTCTGCACGTTAACTGAGGCTCCTCTGAGATGTTAGG 5535		
QY	2221	TAGAGCTTGGACTCTGCACGTTAACTGAGGCTCCTCTGAGATGTTAGG 2280		
DDB		2221 TAGAGCTTGGACTCTGCACGTTAACTGAGGCTCCTCTGAGATGTTAGG 2280		
QY	5536	GAAGCTTAACTGAGGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCT 5595		
DDB		5536 GAAGCTTAACTGAGGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCT 5595		
QY	2281	GAAGACTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCT 2340		
DDB		2281 GAAGACTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCT 2340		
QY	5596	CCCTGAGCTGGGATTTGGGTTGGGGACCTGAGTTCCTCTGGGGAGCTGATGT 5655		
DDB		5596 CCCTGAGCTGGGATTTGGGTTGGGGACCTGAGTTCCTCTGGGGAGCTGATGT 5655		
QY	2341	CCCTGAGCTGGGATTTGGGTTGGGGACCTGAGTTCCTCTGGGGAGCTGATGT 2400		
DDB		2341 CCCTGAGCTGGGATTTGGGTTGGGGACCTGAGTTCCTCTGGGGAGCTGATGT 2400		
QY	5656	AATGATCCTGGGGATCC 5674		
DDB		5656 AATGATCCTGGGGATCC 5674		
QY	2401	AATGATCCTGGGGATCC 2419		
DDB		2401 AATGATCCTGGGGATCC 2419		

MAGE-1 antigens. Compsns. containing these peptides can be administered, as a vaccine to patients susceptible to MAGE associated tumours, e.g. melanomas.

Db	1118	ATACCCGGCCCAGAAAAGGATGCCAACAGACTGGAAAGTAATTGTCTTAGCTC	1177
Qy	2471	TAGGGGACCAGGATGCCAACAGACTGGATGCCAACAGGAGAA	2530
Db	1178	TGGGGAACTGTCAAGGATGCCAACAGGAGAG	1237
Qy	2531	GTGGGGCCCMGGAGATGGGCTTGGGTTAAGGGGGATGTCATATGCA	2590
Db	1238	GTGGGGACCCCTAGGGAGATAAGGGGTTAAGGGGGATGTCATATGCA	1297
Qy	2591	GGAAATTGGGTGAGAACAGGGGTGAGGATAAAGATAGTGAGACACA	2650
Db	1298	GGGGTTCCCTGTAGAAAGGGCAGTCGGCAGGATAAGATGAGAACCRAGG	1357
Qy	2651	GGGATATTGAAATCCACCCCCGAAACCAAAGGGTCAACCTAACCCAGGA	2710
Db	1358	AGGCATATAAGTTCAACCTAACCCCTGGACCTAACCCAGGA	1417
Qy	2711	T-----GTGGCTTCATTTCACTCTGTTICAGATCTGGCGAGGTGAGCACCTCAT	2763
Db	1418	TACAGGATGTGGCCCTCTCCTACTTTCAGATCTAGGGAGTTGACCTGT	1477
Qy	2764	TCTCAGGGGTGACTCAAGTCAAGGACCCATCTGGTCTAAAGACAGGCGTC	2823
Db	1478	TTCAGAAGGTGACTCAACACAGGGG--CCCTCTGSGCAGACATGTT	1534
Qy	2824	CCAGGATCTGGCTGGTCTGGGAAACATAGGGAGGACTGAGGTACCCAGGAC	2883
Db	1535	CTTGGATCTGCCAGCATCCAGTGGACTCAACACAGGGG	1594
Qy	2884	CAGAACACTG-AGGGAGACTGCCAGAAATCACCCCTGCTCACCCAGAGAG	2942
Db	1595	CAGATGAGGAGGCTGGCTGGGAACTATAGGGAGGACTGAGGTACCCAGGAC	1654
Qy	2943	CATGGGCTGGCCGTCTCCGAGTCTCCGATCTATGATCAGGGAC	3002
Db	1655	CTTGGCAGGGCTGTCAGTGAAGTCCCTCCATAT-CTGGGATCTGAGTCAGGGAA	1713
Qy	3003	GGGAGGCTGGTCTGAGAACGGCTAGGGTCAAGGAGGCTGGCC	3062
Db	1714	GGGAGGCTGGTCTGAGTCAAGGGCTGAGTCAAGGGGGCTCAGGGCT	1773
Qy	3063	GCCAGGAGTCAAAGGTGAGCACCAAGGGGCACCTCACCCAGGACATAATTCAATGA	3122
Db	1774	GCGAGGTGAGGTGAGCACCAAGGAGGACTCCACCCAGAACCTGGACTCAATGA	1833
Qy	3123	ATTTGATATCCTCTGGCTGCCCTTCCCAAGGACCTAGGCAGATGTTGT	3182
Db	1834	A-TTGTGACATCTCTGTTCTGAGTCAATGAGGACCTGTCAGTGTGGGT	1892
Qy	3183	CCCTCT-CCTGCTTCCATGGGATCTATGGGATCTATGAGTCTGAGTCTCA	3239
Db	1893	CCCTCTPATCTCTCTGTTCTGAGTCAATGAGGACCTGTCAGTGTGGGT	1952
Qy	3240	GACCAAGAAAAGGGCAGGATCAGGGCCCTGGAGAAAATAAGGGCCCTGCTGAGA	3299
Db	1953	AGCAGCAAAGGAGGACTGGGCTTACAGGAGAAAGGTGAGGGCTGAGT	2011
Qy	3300	ACAGAGGGGGTCACTGCCACTGGCTGAGTGGGATGTCACAGTCAGCCCT	3359
Db	2012	ACAGAGGGGACCTCCACCCAATAGACTGGGACCTCACGGATCTGCTGC	2071
Qy	3350	GTAAGCTGAGAACGGCTGGCTGAGGCTGGCTGGCTGAGGCTGGATGTT	3419
Db	2072	GACACTCTGGGATCTGGTGTGAGTCACTGAGCTGAGTCAGTCAGCTG	2131
Qy	3420	TCTTCCT----GGACCTCAGGAAACGGCAGTGGCTGAGCACTATC	3472
Db	2132	TCTCCAGGAACTAGGAGCTCAGGAAACGGAGTGGCTGAGT	2190
Qy	3473	CTAGGTACAGGACAGGGATCACAGGGTGTGCAAGCTGAGTGGCTGATG	3532
Db	2191	CTAGGTACAGGACAGGGAGGAGCACAGTCACAGTCAGTCACAT	2250

Qy	3533	CACACCAAGGGCCCACCTGCCAACAGAACACATAGGACTCCACAGAGTCCTGGCTCTCA-C	3591
Db	2251	CACACCAAGGGCCCACCCGCC-CAGAACAAATGGGACTCCAGAGGGCTTGGCTCTCAC	2309
Qy	3592	TCCCTACTGTGCACTCTGAGTCAATGACCTCTGCTGGCCGCTGACTCCCTGA	3650
Db	2310	TCCCTATTCCTCAGTCAGCTGAGCTGACATGTCGGCTGTAACCTGAGGTGCCCCT	2369
Qy	3651	CTCACTTCCTCCCTAGTTICA-GGGACAGGCCAACCCAGGAGATTCCCTG	3709
Db	2370	CCCACTTCCTCCCTAGTTCTGAGGGGACAGGTGACAAAGTAGGACCCGGGACTG	2429
Qy	3710	AGCCACAGGAGCACCAAGGAGAACATCTAAGTAGGCTGTTGTTAGACTCTCCAAAG	3769
Db	2430	AGGAGCATG-----AAGGAGAACATCTAAGTAGGCTTGTCAAGGCTCTCAAG	2481
Qy	3770	GTTCTCAGCTGAGGCTGAGGCTCTCCTCACACACTCCCTCTCCCAGGCC	3824
Db	2482	GTCACTGTCAGTCTGCTCACTAAGGCCCTCACACAGCCTCTCCTCCCAGGCC	2541
Qy	3825	TCTTCATGGCCAGCTCTGCCACACTCTCCTCTGCTGAGGAGTCATCATGT	3884
Db	2542	TCTCTCATGGCCAGCTCTGCCGCACTCTCCTCTGCTGAGGAGTCATCATG	2601
Qy	3885	CTCTTGAGCTAGAGAGACTGCTGAGCTGACTGAGCTGAGCTGAGGCTTGA	3944
Db	2602	CTCTGGCCCTGGCTGGTGGCTGGAGGCTCTGGCCGAGGAGGAGGAGG	2661
Qy	3945	CCCTGGCCCTGGCTGGTGGAGGAGT-----GCAACCTCCCTCTGAGGAG	3983
Db	2662	CCCTGGCCCTGGCTGGTGGCTGGAGGCTCTGGCTACTGAGGAGCACG	2721
Qy	3984	CTCTCCCTCTGGCTGGGACCCCTGGAGGAGGCTGCCAACAGATCCTC	4043
Db	2722	CTCTCATCTACTGGAAGT-----TACCTGGAGCTACCTGAGGAGTC	2781
Qy	4044	CCAGAGTCCTAGGGAGCTGGCTGGCTGGAGGAGCTTCACTTCACTC	4103
Db	2782	CCCACTCTCAGGGAGCTCAGCTCTGAGCTACATCAACTACATCTAC	2841
Qy	4104	AACCACTGAGTGGGGCTCCAGCAGCCGTTGAAGGAGGGCCAGGACCTCT	4163
Db	2842	AATCCGTATGAGGGCTCCAGCAGCAACCAAGGAGGGCCAGAAGGAGG	2901
Qy	4164	AGTCCTGCTGGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTGTG	4223
Db	2902	AGTCGGATCTCAAGGCAACATGAGGAATGTTGAGTGGTCACTTCTG	2961
Qy	4224	TCAAATTCGACCCAGGGCTCAAGGCAACATGAGATCTGGAGTGTCA	4283
Db	2962	TCAAGATCTGAGCCAGGGCTCAAAAGGAGAAATGTTGAGTGGTCA	3021
Qy	4284	ATTACAGCAGTCAGTGGCTGGAAAGGCTCTGAGTCTTGGAGTGT	4343
Db	3022	ATTGCCAGGACTCTCTCCGTGATCTTCAGCAAAAGCTCCAGTACTG	3081
Qy	4344	TGGCATTGACTGAGGAAAGGAGGCCACTCTCTATGTCCTGTCACCTG	4403
Db	3082	TGGCATGAGGGCTGAGTGGTCACTGAGCTGAGTCACATGTCACCTG	3141
Qy	4404	TAGGTCTCTCTATGATGGCTGCTGGTGTGATAATCAAGATCATGCC	4463
Db	3142	TGGGCTCTCTCTAGATGGCTGCTGGTGGAGTGGTCACTGAGCTG	3201
Qy	4464	TGATAATTGCTCTGGTCTGAGTGGCTGAGTGGCTGAGGAAATCT	4523
Db	3202	TGATAATTGCTGGCCATTAATGCGCAATAGGGGACTGTCGGCTG	3261
Qy	4524	GGAGGAGCTGAGTGTGAGTGGAGGTGATGGAGGAGCACGTGCT	4583
Db	3262	GGAGGAGCTGAGTGTGAGTGGAGGTGAGGGAGGAGGAGGAGG	3321

Db	2722	CCTCTACTCTAGTGGAAAGTACCCCGGGAGGCTGCCTGTGCCGACTCACCGAGTCCTC	2781	Db	3801	ATGACAGTAGTCACACATAGTCAGTGGTCTGTTATAGTTAGGGTAAGAGTCCTGTTTTA	3860
Qy	4044	CCAGAGTCCTAGGGAGCCTCCGCTTCCCACTCAACTCACTCCACTCGACAGAGCC	4103	Qy	5119	TTCACTATGGAAATTCCATTCATTTGTCATTGTCATTGTCATTGTCATTGTCATTG	5176
Db	2782	CCACAGTCCTAGGGCTCCAGGCCCCCTCACTACATCACTCTGGAGAC	2841	Db	3861	TTCACTATGGAAATTCCATTCATTTGTCATTGTCATTGTCATTGTCATTGTCATTG	3920
Qy	4104	ACCCCAGTGAGGTTCAGGCCCCTGAAAGAGGGCCAAGGCTCCGACCTCTGTGATCCTGG	4163	Qy	5177	GTACTTAAATGATGAGCAGTAAATAGATGAGATAAGAAACTAAAGAA	5232
Qy	4224	TCAAATATCGAGGCCAGGTCAACAAAGCAGAAATTGCTGGAGAGTGTCACTCAAA	4283	Qy	5293	ATAGAGAAGTAGTCATTTGTCCTGCTTATACCTGTCATTGTCATTGTCATTGTCATTG	5292
Db	2962	TCAACTATCGAGGCCAGGTCAACAAAGCAGAAATTGCTGGAGAGTGTCACTCAAA	3021	Db	3921	GTATTGCGCTATATGTCAGGAAATTACATGATACAAGGAAAC	3974
Qy	4284	ATACAAAGGACTGTTCCTGAGCTAACTAACTAGAAGGCTGCTGATTGGTTGGCTTCGTC	4343	Qy	5293	ATAGAGAAGTAGTCATTTGTCCTGCTTATACCTGTCATTGTCATTGTCATTGTCATTG	5292
Qy	4344	TTGGCATGAGGTGAAGGAGGAGAACGAGAACCTCTGAGTCACCTGCTGGTCT	4403	Db	3974	-TCAGAGATGAGTAAATTCTGCCTTATACCTGTCATTGTCATTGTCATTGTCATTG	4029
Db	3022	ATGCCAGGACTCTTCCTGGTACATCTTCAGCAAAGCCCTCGAGTACTGAGCTGGTCT	3081	Qy	5293	ATAGAGAAGTAGTCATTTGTCCTGCTTATACCTGTCATTGTCATTGTCATTGTCATTG	5292
Qy	4524	GGAGGAGCTGAGTGTGAGTGGCTGATGAGGGAGGACAGTGGCTATGGGGAGC	4583	Db	4030	ATGTTGATGTTGTCCTGTCATTTGTCATTGTCATTGTCATTGTCATTGTCATTG	4080
Db	3262	GGAGGAGCTGAGTGTGAGTGGCTGATGAGGGAGGAGAACCTGGGAGGAGACAGTGG	3141	Qy	5353	AAGAAATTCTTCCTGTCACCTGGCTTTCATCCATGACTGAGCATGCTTTGG	5412
Qy	4643	CGAGAGTGTGTCACCCAAAGATTTGGCTGGTGTATAATCGATCATGCCAAGACAGGGCTCC	4643	Db	4081	--AATCTCTCTGTCATGGCTACGGCTCATTTTACCATGTCATTGTCATTGTCATTG	4137
Db	3142	TGGGCTCTCCCTACATGGCTGGCGSACAACTCAGGTCATGCCAAAGACGGCTCC	3201	Qy	5413	AGGGCCTGG	5422
Qy	4464	TGATATTGTCCTGGTCATATGGCAATGGAGGGGGCATGTCCTGGAGGAAATCT	4523	Db	4138	AGGGCCTGG	4147
Db	3202	TGATAATCGTCTGGCCATTAATGCAAAATAGGGGACTGTGCCCTGAGGAAAATCT	3261	RESULT	11		
Qy	3262	GCTAATGTAAGTCTGGTCAATGAGGAGGAGAACCTGGGAGGAGAACCTGGGAGC	3321	X26974			
Db	3322	CCAGGAGCTGCTCATGCAAGATCTGGTCAAGAAACTACCTGGAGTACGGAGGTGC	3381	ID			
Qy	4763	CATCCCCTGGCTGAAAGCAGCTTGGAGGAGAAAGTAGCTGGAGATAAGCTGGAGA	4822	AC			
Db	3502	CACCCCTGCTGAAAGGGCTTGGAGGAGAAAGTAGCTGGAGTACGGAGGTGCAG	3561	DT			
Qy	4823	CCAGGCCAGTGGAGGGACTGGCCAGTCAGTCAGTCAGTCAGTCAGTCAGTC	4882	DE			
Db	3562	CCAGGCCAGTGGAGGGCTGGCCAGTCAGTCAGTCAGTCAGTCAGTCAGTC	3621	CDNA			
Qy	4883	CCCTGCTCTGGTGCATGAGGCAGAGGAGGGCTAGTGTCTTC	4762	CDNA			
Db	3622	CCACIGCCCTGGTGCATGAGGCCATTCTGCCTCTGGTGCATGAGGCCATT	3501	CDNA			
Qy	4941	TCTAGTAGTGTGTTCTGTTCTATGGGTGACTTGGAGATTATCTGGTCTTGG	5000	PI			
Db	3682	TTAGCAGTAGTGTGTTCTGTTCTATGGGTGACTTGGTCTTGG	3741	Pi			
Qy	5001	ATGTTCAAATGTTCTTAAAGGATGTTGACTTCAGTCAGTTATGCAAGTTATGA	5060	DR			
Db	3742	ATGTTCAAATGTTCTTAAACATTGGTGAACATTCAAGTTATGA	3800	DR			
Qy	5061	ATGACAGCAGTCACAC--AGTCGTGTATAGTTAAAGGTAAGGTGTTGTTTTA	5118	PS			
Qy				Query Match	31.1%	Score 1762.6;	
				Best Local Similarity	81.0%	Pred. No. 0;	
				Matches 2315;	Conservative 0;	Mismatches 474;	Indels 68;
							Gaps 20;
Qy				Qy	2790	AGGAGCCCATCTGGCTTAAAGACAGAGGGTCCAGGATCTGCCATGGCTTGGTGA	2849

Db	1365 AGGGCCCCCTATGTGGAGCATGTCAGTGGTCCAGGATCTCCAAACCTCATCGGTGA 1424
Qy	2850 GGACATGGGGAGCACTGGGTACAGGCCAGGACACACTGA -GGGAGACTGCGACAG 2908
Db	1425 AGACATGGGGAGATTGGGTACCCCTGGGACAGATGGCACTGGGGCCCATAA 1484
Qy	2909 AAATAGGCCCTGGCCTGTGTCACCCAGAGACCATGGGCTGTCGGGAGGGTC 2968
Db	1485 AAATGTGCCCTGCTCTGTTACCTAGAACCTCTGAGGGCTGAGCTGGTC 1544
Qy	2969 CCTCGTTATCCTGGATCATTGATGTCAGGGGGGCCCTGGCTGAGAAGGCTG 3028
Db	1545 CCTCAATTATCCTAGATACTGTAGGGAGGGAGCCCTGGCTGAGGGCTG 1604
Qy	3029 CGCTAGGTCAGTAGAGGGCGTCGCCAGGAGCAAGGTGAGGACAAAGC 3088
Db	1605 CACTGGCAGTAGGGAGGCTCTCACGCCCCTACTGGAGCTGGAGTGGACAAAGC 1664
Qy	3089 GGGCACCTACCCAGACACATTAAATCCAATGAAATTGGACATCAATAATTGGACA 3147
Db	1665 AGTCCTCTACCCAGGGTACATGGACTCAATAATTGGACA 1724
Qy	3148 CCCAGGACTTAGGCACCTGGCAGATGTTGTCCTCCCTGTCCTCCATTCTCTAT 3207
Db	1725 CGGGGACCTGGGATGTGGCGAGATGGCTCCCTCATGTTTCTGACATPAT 1784
Qy	3208 CATGGATGGAACCTTG - ATTGGATTCCTGAGCAGCAAAGGGAGGATCAGGC 3265
Db	1785 CAGGTATGAGTCTGACATGAGATTCCTGACATGAGAAGGGGGAT-TAGGC 1843
Qy	3266 CCTGCCAGGAAAATATAAGGGCCCTGGTGGAGAACAGAGGGGTCACTCCATGAG 3325
Db	1844 CCTTAAGGAAAGTGAGGGCTGTAGTGAGAACAGGGGATCCACCTGGTAG 1903
Qy	3326 AGTGGGATGTCACAGAGCAGGCCACCCCTCTGGTGGACTGAGAACCCAGGGCTGTG 3385
Db	1904 AGTGGGACCTGGCCAGAGCTGGCAACCCCTCTGACACTTCTGGAAATCTGGCTCGG 1963
Qy	3386 CTGGGCTGACCTGACCCTGAGGGCCGIGGATTCCTCTCTGGGCTGAGGCTCAGGA 3438
Db	1964 TTGCTGTCTGCACATTGGGGCCCTGTGGATTCCTCCAGGAATACTGGAGCTCAGGA 2023
Qy	3439 ACCAGCAGTGGCCAGGAGCTGGCTGAGACAGTATCTCAGGTGAGGGATGGCAC 3498
Db	2024 ACAGGACTGAGGACTGGCTGAGCTGGCTGAGGAGCTGGCTGAGTAAGGGGCTC 2083
Qy	3499 AGGGTGTGGCCAGGAGCTGGCTGAGCTGGCTGAGACAGTATCTCAGGTGAGGGAG 3558
Db	2084 AGATAGTGGCAACGGTGAAGGTTGCTGGATCAAACCAAGGGCCCCACCTGCGACAG 2143
Qy	3559 GACACATAGGACTCACAGCTGCTGCTCA -CTCCCTACTGTCAGTCTGAAATCTG 3617
Db	2144 AACACAT -GAGCTCAGGGCTCTGGCTCACCTCAACTTCTACTGTCAGGCTCTCA 2202
Qy	3618 ACCCTCTGCTGGCCGGCTGTACCCCTGA -GTACCCCTCTCACTTCCCTCTCAGGTTTCTCAGG 3676
Db	2203 GCATGCGTGGCCGATGACCCCTGAGGTTGGCCCTCTCACTTCCCTCTCAGGTTCTGAG 2262
Qy	3677 GGACAGGGCAACCCAGAGGACAGGATTCCTGGAGGCCACAGGGAGCACAGGAGAG 3736
Db	2263 GGAGAGGTGACCTGGAGACCAAGGGCCCCGGAGGACTCTGAGGAGGAGGAG 2315
Qy	3737 ATCTGTAAGTAGGCCTTGTAGTGTCAAGG - - -TCAGTCTCAGCTGAGGGCT 3791
Db	2316 ATCTGTAAGCTCTCAGGCTTGTAGGCTTCAAGSTCCATTCTGAGTCTGGCTCT 2375
Qy	3792 CTCAACACTCCCTCTCAGGCCCTGGGCTCATGGCACTGGCCACAC 3851
Db	2376 CTCAATGTCCTCTCAGGCCCTGGGCTCATGGCACTGGCCACAC 2435
Qy	3852 TCCGGCCCTCTGCTGCCCTGAGAGCTCATGTCCTCTGAGCAGGGACTCTCACTGCA 3911
Db	2436 TCCGGCCCTTGTGGCTTGTAGGAGCTCATGGCACTGGCCACAC 2495

Qy	899	AGAGGGGGGAAAGCACCTGGCTGAGCAGTCCTGGATAAGCACTCACTA	958
Qy	4191	AGAAGGGCGTGAATTGGTTCTCTCAATATCGCCAGGGGCCAGTICA	4250
Db	959	ACAAAGGGGATAGTGCTCATTTTCGCTCAAGTATCGCAAGGGCTGCTCA	1018
Qy	4251	CAAGGGAGAAATGCTGSGAGGTGTCATCAAATTAACGACTGTTCTGAGACT	4310
Db	1019	CAAGGGCGAAATGCTGAGAGTCATCAAATTAACGCTGTTCTGTGATCT	1078
Qy	4311	TGCGAAAGCCCTGTCGASTCTTGCGATTGACGTGAGGAAGCACC	4370
Db	1079	TGCGAAAGCCCTGAGTCCTGGATGAGTGGATGAGGTGGAC	1138
Qy	4371	CCACCGGCCACTCTTCTAGTCCCTGTCACCTGCTTAGGTCCTCTATG	4430
Db	1139	CGCCAGAACCTACACCCCTGTCACCTGGGCTCTCTATGCGCTGCG	1198
Qy	4431	GTGATAATCAGATCATGCCAGACAGGCCCTCTGATGTCATGTC	4490
Db	1199	GTAATAATCAGATCTTCCCAGACAGCCCTCTGATPATGTCGCAATGCA	1258
Qy	4491	TGAGGGGGCCATGCTCTGAGGAGGAAATCTGGAGGTGAGTGTGATGGAGGTGT	4550
Db	1259	TGAGGGGGACAGGCCCTGAGGAGGAATCTGGAGGTGTGATGGGGGTG	1318
Qy	4551	ATGATGGGGAGGACAGTGCCTATGGGAGCCAGAACGGTGTGACCAAGATTTG	4610
Db	1319	ATGATGGGGAGGACACTGCTATGGGACCCAGAAACTGCTACCCAGATGG	1378
Qy	4611	TGAGGAAAAGTACCTGGAGTACCTGGAGTACGGAGTCCTGGCTATGAGT	4669
Db	1379	TGAGGAAAACACTGGAGTACCTGGAGTACGGAGTAACTCGCGGTATGAGT	1438
Qy	4670	TCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAAGCTATGTAAGTCCTGAGTATGAGT	4729
Db	1439	TCTGTGGGGTCCAAGGGCTCTGGCTGAACAGCTATGTAAGTCCTGGCTG	1498
Qy	4730	TCAGGTCACTGGCAAGACTGGTGTGTTCTCCATCCCTGGTGAAGCAGCTTGAG	4789
Db	1499	TCAGGGTCAATGCAAGGTGGCAAGCTGGGACCCAGAAACTGCTACCCAGATGG	1558
Qy	4790	AGAGGAAGGGAGGACTCTGAGCATGAGTGGCTGACCCACGGCACTGGAGGG	4845
Db	1559	AGAGGAAGGGAGGACTCTGAGCATGAGTGGCTGACCCACGGCACTGGAGGG	1618
Qy	4846	GCCCCACTGCACTTCCAGGGCGTCAGGAAGCTCCCTGGCTGACATGAGG	4905
Db	1619	GGCCCACTGCACTAACAA-GCCCTGTGGCAGAGCTCCCTGGCTGACATGAGG	1676
Qy	4906	CCATTCTCACTC---TGAGAGAACGGCTGAGTTCTGTTGAGTGTGTTGAG	4961
Db	1677	CCATTCTCACTCTGTGAGAAATAGCTAGTGTCTTGTAGTGGTTCTTATTT	1736
Qy	4962	ATGGGGTCACTGGAGGATTATCTTGTCTCTTGGAAATTGTCATAATGTTTT	5021
Db	1737	GTGGGAGACTGGAGATTACCTGTTGAGTGTGTTTACGATGTAATGTTAGAATGTT	1795
Qy	5022	AGGGGGGTTGAATGACTCAGCATCCAAGTTTAAATGACAGCAGTCACAGTC	5081
Db	1796	ATGGATGGTCAATTACTCAGCATCCAACATTGAGTTAACCTTAAATGTC	1855
Qy	5082	TGTTATATGGTTAAGGGTAGAGCTGGTTTATCGATGGAAATCCATTCA	5141
Db	1856	TGTTATATGGTTAAGGGTAGAGCTGGTTTATCGATGGAAATCCATTCA	1915
Qy	5142	TTTGTGAAATGG---ATAATAACAGCAGTCAGTAAAGTACTTAGAAATGAAAAATG	5198
Db	1916	TTTGTGAAATGGACATAAACAGCAGTCAGTAACTTAACTTAACTTAACTTAA	1972
Qy	5199	ACAGTAAATGAGATAAGAACTAAGAAATAGAGATACTGCAATCTGGCT	5258
Db	1973	CACCGTGAATGGGAT---AAATGGTGGAT-----	2020
Qy	5259	ATACCTCAGCTCTATTCTGAAATTATGCTATACTGGATACTGGATTTCCTGGCT	5318
Db	2021	ATGCTCAGCTCTATTCTGAAATTATGCTATACTGGATACTGGATTTCCTGGCT	2080
Qy	5319	TCTTGAGATGTAGAGAAATTAAATCTGAAATAAGAAATTCTCTGTCACCTGGCT	5378
Db	2081	TC---GTGATGTAGAGAAATTAAATCTGAAATAATTAATCTCTGTTAACCTGGCTCA	2137
Qy	5379	TTTCCTCTCCATGCACTGACCATCTGCTCTGGGTTAGTGGAGATG	5438
Db	2138	TTTCCTCTCTATGACTGAGCATCTGCTCTGGAGGCTCTGGAGTGTGAGATA	2197
Qy	5439	CTAAGTAAAGCCAGACTCATACCCCATAGGGCTCTAGAGTCTAGGAGCTGAGTC	5498
Db	2198	CTAAGTAAAGCCAGACACACACCTACAGTAGGGTATAAGAGTCTAGGAGCGCTG	2257
Qy	5499	GTAAATCAGCTGGAGAAGTGGCCCTAAGATAGTGGAAAGAGTCAAGAGGGTGA	5558
Db	2258	ATRATTAAAGGTGACAAGTGTGCTCTAGATGAGGAAAGT---AAGCAGTGTGG	2313
Qy	5559	TGTTGGGGCTCCGGGTGAGAGTGGTGTGAGTCATACTGGCTGAGCTGGG	5618
Db	2314	TATGGGGCTCAGGTGAAGTGGTAATTCCCTGTG-TGGGGCTTGTG	2372
Qy	5619	TGGGAAACTGTGACTCTCCCTCTGGGGACTGTATGTAATGTCGGGGATCC	5674
Db	2373	TGTTGGAAACTGCAATTCTCTGAGGACTGATCTGTTGGGGTCC	2428
RESULT 13			
Q72483			
ID		standard; DNA: 2531 BP.	
AC		Q72483;	
DT		22-JUN-1995 (first entry)	
DE		Tumour rejection antigen MAGE-41 gene	
KW		melanoma antigen; melanoma	
KW		cancer; cytotoxic T cells; antigen D; human leucocyte antigen; Homo sapiens.	
OS			
PH		Location/Qualifiers	
FT		Key	
FT		cds	
		/tag= a	
FT		625..158	
FT			
PN		W09423031-A.	
PD		13-OCT-1994.	
PR		002877.	
PR		26-MAR-1993; US-037230.	
PA		(LUDWIG INSTITUTE FOR CANCER RESEARCH).	
PI		Boon falleur T, Gaugier B, Van DER EYNDE B,	
DR		WPI: 94-333192/41.	
PT		New tumour rejection antigen precursor MAGE3 - useful in treatment and diagnosis of cancer	
PS		Disclosure; Page 68; 10pp; English.	
CC		Q72483 is the gene which contains the coding sequence for melanoma antigen-1 (MAGE-41). Another melanoma antigen MAGE-3 is encoded by Q72470, this is a tumour rejection antigen precursor. Melanomas characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytotoxic T cells specific for the complex of antigen D (the mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-AL).	
SQ		Sequence 2531 BP;	
Query Match		Score 1678.8;	
Best Local Similarity		DB 1: Length 2531;	
Matches 2074;		Pred. No. 0;	
Mismatches 0;		Mismatches 317; Indels 65; Gaps 1	
Db		GGATCCAGCCCCCTCCAGAAAAATAAGGGGCTGAGAACAGGGGGTCATCC	3315
Db		1 GGATCCAGCCCCCTCCAGAAAAATAAGGGGCTGAGAACAGGGGGTCATCC	60

Db	2198	CTAGGGTAAGCCAGACACACTACCGTAGGGTATTAAAGATCTAGGAGCCGGTCA	2257		QY	3436	GGACCAGGCACTGAGGCCCTGGTCTGAGACACTATCCTCAGGTACAGAGGAGGATG	3495
Qy	5499	TGAACTCGAGGTGGCAGAAGTCCTCTAAAGATUTAGGGAAAGTGAAGAGGGCTGAGGG	5558		Db	181	GGAAACAAGCCAGTGGCCCTGGTCTGAGACACTGTCCTCAGTTACAGAGGAGGATG	240
Db	2258	ATAATAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2313		Qy	3496	CACAGGGTGTGGCAGACTGAAGTCAAGTGCTCAATAGTGAATGTTCCCTGAATGCA	3555
Qy	5559	TGTGGGGCTCGGGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG	5618		Db	241	CACAGGTGTGGCAGACTGAAGTCAAGTGCTCAATGCAACCAAGGGCCCCACCTGCA	300
Db	2314	TATGGGGCTCAGGTGAGACTGGTGGGGTGTAAATTCCCTGTG-TGGGCCCTTGGGCT	2372		Qy	3556	CAGGACATAGGACTCCAGAGTCTGGCCRAACCTCCCTACTGTGCTGTTGAGAT	3615
Qy	5619	TRGGAAACTGAGTGTGGAGCTCCCTGTGGGGAGCTGTGGTGTGGTGTGGTGC	5674		Db	301	CAAGACATAGGACTCAAAAGTGTGGCCCTACCTCTAACCATCAATCCCTGAGAT	360
Db	2373	TRGGAAACTCATTTCCTGTGGGGAGCTGTGATCTTGTGAGCTTGTGTC	2428		Qy	3616	CGACCTCTGCTGGGGCTGTGACCTGTA-GTACCCCTCACTTCCTCTCAGGTTCA	3674
	RESULT	14			Db	361	CGACCTCTGCTGGGGCTGTGACCTGTCCTCAGTTCCTCTCAGGTTCA	420
Q3 2357		standard; cDNA: 2531 BP.			Qy	3675	GGGACAGGCAACCCAGAGGAGGATTCCCTGGAGCACAGGGCAGCAAGAGGA	3734
AC	Q3 2357		(first entry)		Db	479	AGATCTGTAAGTAAAGCTGTGTTAGAGCTCAAGTGGTCTCAGTGGTCTC	538
DT	22-APR-1993				Db	421	GCAGACAGGCCAAC - -GAAGACAGGATCCTGGAGGCACAGGGCACAAAGGAA	478
DE	MAGE-4 gene.				Qy	3735	AGATCTGTAAGTAAAGCTGTGTTAGAGCTCAAGTGGTCTCAGTGGCCACACTC	3854
KW	melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;				Db	539	ACACACTCCCTCCTCCCAGGCTCTGGTCTCATGGCCAGCTCTGCCAGT	598
KW	tumor rejection antigen precursor; MAGE; antigen E; gene family; ss;				Qy	3855	TGCCTGCHNCCNGACAGAGAGTCATGTGCTGTGAGGAGTGCAGTCAGTC	3914
OS	Homo sapiens.				Db	599	TGCTGTGCTGCCCTGACCAAGTCACTGTCTCTGAGCAGAGTCAGTCAGTC	658
Key					Qy	3915	CTGAGAACCCCTTGAAGGCCAACAGAGGCCCTGGCTGGCTGGCTGGCT	3974
FT	Location/Qualifiers				Db	659	CTGAGAACGGTGAAGGCCAACAGAGGCCCTGGCTGGCTGGCTGGCT	718
FT	625..1578				Qy	4010	-----CCTCTCCCTCCTCCTCCTGGGACCCCTG	4010
PN	/ *tag= a				Db	719	CTACTGAGGAGGAGGGTGGCTCTCCCTCTGGTCTGGCTGGCTGGCT	778
PD	WO920356-A.				Qy	4070	CTGAGGAGGGCCAAGGACTCTGGAGTCTGAGTCTCAGGAGCTCCTGGCT	4070
PD	26-NOV-1992.				Db	839	TACCCACTTCCCTCTGGTCTCTCTCTGGAGGAACCCATAGGGTTCAGGCCAG	898
PF	22-MAY-1992;	004354			Qy	4131	AAGAGGAGGGCCAAGGACTCTGGAGTCTGAGTCTCAGGAGTAACTACA	4190
PR	23-MAY-1991;	US-705702.			Db	899	AGGAAGTGGCTGTGCTGAGTCACTGGCTCTCCAGAGTCTGGGCTCTG	958
PR	09-JUL-1991;	US-728338.			Qy	4191	AGAGGTTGGCTGTTGGTGTGGCTCTCTCTGGAGGACCCAGCTGA	4250
PR	23-DEC-1991;	US-764164.			Db	959	ACAAGGTGGATGATGATGATGATGATGATGATGATGATGATGATG	1018
PA	(LUDWIG) LUDWIG INST CANCER RES.				Qy	4251	CAAAGGAGAAAGCTGGGCTCATCAAATTAAGGAGGTTCCCTGGAGAGCT	4310
PI	Boon T, Chomez P, De Plaein E, Lurquin C, Traversari C;				Db	1019	CAARGGCAGAAAGCTGGGAGAGTCATCAAATTAAGGAGGCTGTTCTGTGATC	1078
PI	Van Den Eynde B, Van Der Bruggen P, Van Pel A;				Qy	4311	TGGCAAACCCCTCTGAGCTTGGCTCTGAGCTCTGCTGAGTCTGAGTC	4370
WPI	92-1546/50.				Db	1079	TGGCAAACCCCTCTGAGCTTGGCTCTGAGCTCTGCTGAGTCTGAGTC	1138
PT	PT	encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis			Qy	4371	CCACGGCCACTCTGAGCTTGGCTCTGAGCTCTGCTGAGTCAGTGGCT	4430
PT	PS	DISCUSSION: Page 79-80; English.			Db	1139	CCGCAGCAACCTACACCCCTGTCCTGCTGAGCTCTGCTGAGTCAGTGG	1198
CC	CC	The sequences given in Q32352..69 represent a new family of genes referred to as melanoma antigens (MAGE). The cDNAs of this gene family were identified during the isolation of the antigen E gene. The MAGE cDNAs, when tested, did not transfer expression of antigen E, but they did show substantial homology to the antigen E cDNA.			Qy	4431	GTTAACTAGATGAGCTGGGCAAGACGCTCTGGTGTGATGATGATG	4490
CC	CC	other and are expressed in tumour cells including several types of human tumor cells as well as in human tumors. MAGE expression is not restricted to melanomas. MAGE refers to a family of tumor rejection antigen precursors. The antigens resulting from these genes are referred to as MAGE TRAs or melanoma antigen tumor rejection antigens. See also Q32351.. Sequence 2531 BP; 608 A; 592 C; 701 G; 630 T;			Db	1199	GTAAATACTAGATCTCCCTGAGCCACATGGTCAATTCGTC	1258
SQ	29.6% Score 1677.2; DB 1; Length 2531;				Qy	4491	TGGGGGGGCCATGCTCTGGAGGAAATCTGGAGGAAATCTGGAGGAGCTGATGGAGGTGT	4550
Best Local Similarity	84.4%	Pred. No. 0;	Mismatches	318; Indels 65; Gaps 14;				
Matches	2 Conservatve	0;						

Db	1259	TGAGGGCGACAGGCCCTCTGGAGGGAAATCTGGAGGGCTGGTGTGATGGGGTGT 1318	Db	2314	TATGGGGCCTCAGGTGAGACTGGTCGGGGTGATAAATTCCCTGTG-TGGGCCCTTGGGCT 2372
Qy	4551	ATGATGGAGGGCACAGTCAGTGCCTATGGGAGCCAGGAGCTGTCACCCAAGATTGG 4610	Qy	5619	TTGGAAAATGGCAGTCCCTCTGGGGGAGGTGAATGTGATCTGGGGGATC 5674
Db	1319	ATGATGGAGGGCACAGTCAGTGCCTATGGGAGCCAGGAGCTGTCACCCAAGATTGG 1378	Db	2373	TTGGAAACTGCATTTCCTGGGACTCTGATTAAGCT 2428
Qy	4611	TGAGGAAAGTACCTGGAGTA-CGGCAGTCCGCCGACATGATCCCACGCTATGAGT 4669	RESULT 15		
Db	1379	TGAGGAAACTACCTGGAGTA-CGGCAGTCCGCCGACATGATCCCACGCTATGAGT 1438	Q32358	standard; cDNA: 2531 BP.	
Qy	4670	TCTGTGGTCAGGGCCTCGTGAAGAACAGCTATGTAAGTGTGA 4729	ID	Q32358; AC	
Db	1439	TCTGTGGTCAGGGCTCTGGCTGAAGAACAGCTATGTAAGTGTGA 1498	DT	22-APR-1993 (first entry)	
Qy	4730	TCAAGGTCACTGCAAGAGTGGCTGTTCTCCATCCATGGTGAAGCAGCTTGTAG 4789	DE	MAGE-E1 gene.	
Db	1499	TCAAGGTCAAAGAACAGTGGCATGCCAACCTCCGTGAAGCAGCTTGTAG 1558	KW	melanoma antigen; MAGE TRA; melanoma antigen precursor; tumor rejection antigen; MAGE; antigen E; gene family; ss.	
Qy	4790	AGGAGGAAGGGAGCTGAGCATGAGTGGCAAGGGCACTGGAGGG----GGACT 4845	OS	Home sapiens.	
Db	1559	AGGAGGAAGGGAGCTGAGCATGAGTGGCAAGGGCACTGGAGGGCT 1618	FH	Location/Qualifiers	
Qy	4846	GGCAGGTGCACTTCAGGGCGCTCAGGTGAGCTGAGTGTGA 4905	Key	Key	
Db	1619	GGCCAGTGCATCTAACAGCTGAGCTCCCTGGAGCACTGGTGA 1676	FT	625..1578	
Qy	4906	CCATCTTCACTC---TGAAGAGGGCTAGTGTCTCATGACTAGTGTCT 4961	PN	/*tag= a	
Db	1677	CCATCTTCACTCAGTTGAGAAATACTGAGTGTCTAGTGTCT 1736	PN	W09220356-A.	
Qy	4962	ATGGGTGACTTGGGATTAATCTCTTGTCTCTTGGGATTGTCAAAGTTTTT 5021	PD	26-NOV-1992;	
Db	1737	GTGGGTGACTTGGGATTTATCTCTTGTCTTACAATTGTGAAATG-TTCTTT 1795	PT	004354..22-MAY-1992;	
Qy	5022	AAGGGATGGTGAACCTGAGATTAATCTCAAGTCAGTCAAGTC 5081	PR	004354..23-MAY-1991;	
Db	1796	AATGGATGGTGAATTAACCTGAGATTCAGTCCAGTTATGATCTGC 1855	PR	09-JUL-1991; US-728338..	
Qy	5082	TGTTGATATAGTTAAGGTAAGAGCTTGTGTTTATCAGATTGGAAATCCATTCTCA 5141	PR	09-JUL-1991; US-728338..	
Db	1856	TGTTGATATAGTTTACAGTAGATGAGCTTGTGTTTATCAGATTGGAAATCCGTCTCA 1915	PR	12-DEC-1991; US-807043..	
Qy	5142	TTTGTGAATTTGGGATTAATACAGCAGTGGAAATAGTAACTTGAAGTGAATAATG 5198	PA	(LUDWIG) LUDWIG INST CANCER RES.	
Db	1916	TTTGTGAATTTGGGATTAATACAGCAGTGGAAATAGTAACTTGAAGTGA--AATT 1972	PI	Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;	
Qy	5199	AGCAGTAAATAGATGAGATAAGAACTAAATAAGGATACTAAATTCTGCTT 5258	PI	Van Den Eynde B, Van Der Bruggen P, Van Pel A;	
Db	1973	CACCGTGAATAGGTGAGAT-----AAATTAAGGATCTTAATCCGCCCT 2020	DR	WPI: 92-41546/0..50..	
Qy	5259	ATACCTCAGTCATTCAGTAAATTAAAGATATATGCAATCCCTGGCT 5318	PT	PT	
Db	2021	ATGCCCTCAGTCATTCAGTAAATTAAAGATATATGCAATCCCTGGCT 2080	CC	Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis	
Qy	5319	TCTTGAGAATGTAAGAAATTAATCTGAAATAAGAATCTCTGGTCACTGCTCT 5378	CC	PT	
Db	2081	TC--GTGAATGTAAGAAATTAATCTGAAATAAGAATCTCTGGTCACTGCTCA 2137	CC	PT	
Qy	5379	TTCTCTCCTAGCTGACTGAGTCACTGAGTCACTGAGTGTGGAGATG 5438	CC	CC	
Db	2138	TTCTCTCCTAGCTGACTGAGTCACTGAGTCACTGAGTGTGGAGATA 2197	CC	CC	
Qy	5439	CTAAGGTAAGCCAGACTCATACCCATAGGTCTAGACTCTAGGGTCACTC 5498	CC	CC	
Db	2198	CTAGGTAAGCCAGACACACTACCTGGGTTACTGAGCTCAT 2257	CC	CC	
Qy	5499	GTAATCGAGGTCAGCAAGATGTCCTAAAGATGTAAGGAGGGTGGAGGG 5558	CC	CC	
Db	2258	ATAAATTAGGTAACAGATGTCCTCTGGAAAGTCTAGGGAAATGGCTGG 2313	CC	CC	
Qy	5559	TGTGGGCTCCGGTGTGAGTGTGGCATTTGGCT 5618	CC	CC	
Qy			Sequence	Q32351..2531 BP;	
Db			SQ	607 A; 593 C; 701 G; 630 T;	
Qy			Query	Query Match 29.5%; Score 1675 6; DB 1; Length 2531;	
			Best Local Similarity	84.4%; Pred. No. 0;	
			Matches 2072; Conservative 0; Mismatches 319; Indels 65; Gaps 14;		
Qy			Qy	3256 GGATCCAGGCCTGCAAGAAATAATAAGGCCCTGCTGGAGAACAGGGGTCATCC 3315	
Db			Db	1 GGATCCAGGCCTGCTGGAGAAATGGGGCCCTGAGTGAACAGCATGGATCATCC 60	
Qy			Qy	3316 ACTGGCATGAGTGGGATGTCAGTCACTGGCTTGTGAGCTGAGAAGGC 3375	
Db			Db	61 ACTCCATGAGTGGGACCTCACAGTCAGCTTGTGAGCTGAGTCAGGGAC 120	
Qy			Qy	3376 CAGGGGTGCTGCTGGCTCTGGCCTGCACTGGATCTGGAGCTC 3435	
Db			Db	121 CGGGGTGCTGCTGGATGTCAGTCTGGCTTGTGAGCTGAGTCAGGGTCA 180	
Qy			Qy	3436 GGACCAAGGCACTGAGCTGCTGGCTGAGCTGAGTCAGTCACTGGAGCT 3495	
Db			Db	181 GGAAACAGGCAGTGGCTGAGCTGCTGGCTACAGTCAGGGATG 240	
Qy			Qy	3496 CACAGGGTGTGGCAGTGAATGTTGCCCTGAAATGCAACCAAGGCCACCCTGC 3555	
Db			Db	241 CACAGGGTGTGGCAGTGAATGTTGCCCTGAAATGCAACCAAGGCCACCCTGC 300	

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